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STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 100243

TO: Vanessa L Ford
Location: cm-1/8A16/8E12
Art Unit: 1645

Aug 4, 2003

Case Serial Number: 10/017168

From: P. Sheppard
Location: CM1-1E03
Phone: (703) 308-4499

sheppard@uspto.gov

Search Notes

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STIC-Biotech/ChemLib

100243

From: Chan, Christina
Sent: Thursday, July 31, 2003 3:35 PM
To: Ford, Vanessa; STIC-Biotech/ChemLib
Subject: RE: In re: 10/017168 sequence search

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
308-3973
CM-1, 9B19

-----Original Message-----

From: Ford, Vanessa
Sent: Thursday, July 31, 2003 2:49 PM
To: Chan, Christina
Subject: In re: 10/017168 sequence search

Please search SEQ ID NO:15. Please include interference searches. Please rush!

Vanessa L. Ford
Biotechnology Patent Examiner
Office: CM1 8A16
Mailbox: CM1 8E12
Phone: 703.308.4735

RECEIVED
JUL 31 2003
STIC

Point of Contact
P. Sheppard
telephone number: (703) 308-4499

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: 8/4/03
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: August 1, 2003, 18:26:45 ; Search time 95 seconds
(without alignments)
54.327 Million cell updates/sec

Title: US-10-017-168-15

Perfect score: 101

Sequence: 1 EVEDVPKVEBPASEREGGER 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mmc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_prodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriaph:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	100.0	348	2 Q9ALV7	Q9ALV7 treponema p
2	101	100.0	393	2 Q9JCA3	Q9JCA3 treponema p
3	101	100.0	428	2 Q9ALV6	Q9ALV6 treponema p
4	101	100.0	432	2 O51953	O51953 treponema p
5	101	100.0	548	2 Q9JCA4	Q9JCA4 treponema p
6	97	96.0	256	16 Q83448	Q83448 treponema p
7	82	81.2	227	16 Q83449	Q83449 treponema p
8	50	49.5	187	10 Q9J1I8	Q9J1I8 arabidopsis
9	50	49.5	193	10 Q9J1I5	Q9J1I5 arabidopsis
10	49	48.5	256	4 Q8WV22	Q8WV22 homo sapien
11	48	47.5	547	16 P95090	P95090 mycobacteri
12	48	47.5	2192	5 Q81BW7	Q81BW7 plasmidum
13	47.5	47.0	792	16 Q8CPY0	Q8CPY0 streptococ
14	47	46.5	266	11 Q9D720	Q9D720 mus musculu
15	47	46.5	280	11 Q8K2B4	Q8K2B4 mus musculu
16	47	46.5	280	11 Q9CY20	Q9CY20 mus musculu

17	47	46.5	308	12 Q98494	Q98494 paramecium
18	47	46.5	650	4 Q81Y36	Q81Y36 homo sapien
19	47	46.5	685	5 Q9J381	Q9J381 caenorhabdi
20	47	46.5	1151	5 Q9XUR2	Q9XUR2 caenorhabdi
21	47	46.5	1159	12 Q9IMX8	Q9IMX8 cercopithec
22	47	46.5	1386	4 Q8C0A3	Q8C0A3 homo sapien
23	46.5	46.0	946	10 Q9LPO9	Q9LPO9 arabidopsis
24	46	45.5	174	10 Q8W325	Q8W325 oryza sativ
25	46	45.5	348	4 Q8N446	Q8N446 homo sapien
26	46	45.5	383	2 Q93CV7	Q93CV7 lactobacill
27	46	45.5	434	10 Q93X74	Q93X74 brassica ra
28	46	45.5	779	4 Q9H348	Q9H348 homo sapien
29	46	45.5	849	11 Q8CG01	Q8CG01 mus musculu
30	46	45.5	853	11 Q8CTC3	Q8CTC3 mus musculu
31	46	45.5	853	11 Q8BK66	Q8BK66 mus musculu
32	45	44.6	99	5 Q23793	Q23793 chironomus
33	45	44.6	99	5 Q23794	Q23794 chironomus
34	45	44.6	178	16 Q92UB5	Q92UB5 thizobium m
35	45	44.6	193	16 Q8PQY1	Q8PQY1 xanthomonas
36	45	44.6	264	16 Q31775	Q31775 bacillus su
37	45	44.6	286	2 Q9ANA3	Q9ANA3 bradyrhizob
38	45	44.6	286	10 Q8L7T9	Q8L7T9 arabidopsis
39	45	44.6	294	10 Q9FRT7	Q9FRT7 arabidopsis
40	45	44.6	379	6 Q9GLI3	Q9GLI3 macropus ru
41	45	44.6	474	17 Q96YS8	Q96YS8 sulfolobus
42	45	44.6	483	12 Q9JGT4	Q9JGT4 northern ce
43	45	44.6	798	5 Q45181	Q45181 caenorhabdi
44	45	44.6	873	5 Q20072	Q20072 caenorhabdi
45	44.5	44.1	243	17 Q8TY79	Q8TY79 methanopyru

ALIGNMENTS

RESULT 1

Q9ALV7 PRELIMINARY; PRT; 348 AA.

AC Q9ALV7;

DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

DE Acidic repeat protein.

GN ARP.

OS Treponema pallidum (subsp. pertenue) (Yaws treponeme).

OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.

OX NCBI_Taxid=168;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CDG2;

RA Liu H., Steiner B.M., Rodas B.;

RT "Molecular characterization of the acidic repeat protein (arp) of Treponema pallidum.";

RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=CDG2;

RA Liu H., Steiner B.;

RT "Acidic repeat protein (arp) gene sequence of Treponema pallidum subspecies pertenue (CDC 2 strain).";

RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF342806; AAK01460.2; -

SQ SEQUENCE 348 AA; 37936 MW; EAA446BD82344592 CRC64;

Query Match 100.0%; Score 101; DB 2; Length 348;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVEDVPKVEBPASEREGGER 20
|||||
Db 128 EVEDVPKVEBPASEREGGER 147

RESULT 2

093CA3
ID 093CA3 PRELIMINARY; PRT; 393 AA.
AC 093CA3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Acidic repeat protein.
GN ARP.
OS Treponema pallidum (subsp. pertenue) (Yaws treponeme).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxId=168;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CDCl;
RA Liu H., Steiner B.M., Rodas B.;
RT "Molecular characterization of the acidic repeat protein gene (arp) of
RT Treponema pallidum."
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF411126; AAL07373.1; -
SQ SEQUENCE 393 AA; 42852 MW; C2D9198AA1BB82B5 CRC64;

Query Match 100.0%; Score 101; DB 2; Length 393;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVEDVPKVVPEASEREGGER 20
Db 133 EVEDVPKVVPEASEREGGER 152
|||||

RESULT 3
ID 09ALV6 PRELIMINARY; PRT; 428 AA.
AC 09ALV6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Acidic repeat protein.
GN ARP.
OS Treponema pallidum subsp. endemicum.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxId=53436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bosnia;
RA Liu H., Steiner B.M., Rodas B.;
RT "Molecular characterization of the acidic repeat protein (arp) of
RT Treponema pallidum."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bosnia;
RA Liu H., Steiner B.;
RT "Acidic repeat protein (arp) gene sequence of Treponema pallidum
RT subsp. endemicum (Bosnia strain)."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF342807; AAK01461.2; -
SQ SEQUENCE 428 AA; 46710 MW; B14ED8A074D43933 CRC64;

Query Match 100.0%; Score 101; DB 2; Length 428;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVEDVPKVVPEASEREGGER 20
Db 128 EVEDVPKVVPEASEREGGER 147
|||||

RESULT 4
ID 051953 PRELIMINARY; PRT; 432 AA.
AC 051953;
DT 01-JUN-1998 (TREMBLrel. 06, Created)

DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Acidic repeat protein.
GN Treponema pallidum.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxId=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nichols;
RA Steiner B.M., Liu H., Rodas B.;
RT "Characterization of an Acidic Repeat Protein from Treponema
RT pallidum."
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF015824; AAB94541.1; -
SQ SEQUENCE 432 AA; 46364 MW; 8FE1E4C55CE46A23 CRC64;

Query Match 100.0%; Score 101; DB 2; Length 432;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVEDVPKVVPEASEREGGER 20
Db 168 EVEDVPKVVPEASEREGGER 187
|||||

RESULT 5
ID 093CA4 PRELIMINARY; PRT; 548 AA.
AC 093CA4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Acidic repeat protein.
GN ARP.
OS Treponema pallidum subsp. pallidum (syphilis treponeme).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxId=161;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nichols;
RA Liu H., Steiner B.M., Rodas B.;
RT "Molecular characterization of the acidic repeat protein gene (arp) of
RT Treponema pallidum."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF411124; AAL07372.1; -
SQ SEQUENCE 548 AA; 59405 MW; 1FE5B5BB04D41D13 CRC64;

Query Match 100.0%; Score 101; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVEDVPKVVPEASEREGGER 20
Db 168 EVEDVPKVVPEASEREGGER 187
|||||

RESULT 6
ID 083448 PRELIMINARY; PRT; 256 AA.
AC 083448;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-WAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical protein TP0433.
GN TP0433.
OS Treponema pallidum.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxId=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nichols;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,

RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
 RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
 RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Uteback T.,
 RA McDonald L., Artach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
 RA Hatch B., Horst K., Roberts K., Sandusky W., Weidman J., Smith H.O.,
 RA Venter J.C.;
 RT "Complete genome sequence of *Treponema pallidum*, the syphilis
 agent";
 RT Spirochaete; -;
 RL Science 281:375-388(1998).
 DR EMBL; AE001220; AAC65422.1; -;
 DR TIGR; TP0433; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 256 AA; 27453 MW; E90329D5A119E76 CRC64;
 Query Match 96.0%; Score 97; DB 16; Length 256;
 Best Local Similarity 95.0%; Pred. No. 6.6e-07;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 EVEDVPKVEPASPAREGGER 20
 |||||
 184 EVEDAPKVEPASPAREGGER 203
 RESULT 7
 083449 PRELIMINARY; PRT; 227 AA.
 AC 083449;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Hypothetical protein TP0434.
 GN TP0434.
 OS *Treponema pallidum*.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; *Treponema*.
 CX NCBI_TaxID=160;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Nichols;
 RX MEDLINE=98332770; PubMed=9665876;
 RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
 RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
 RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
 RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Uteback T.,
 RA McDonald L., Artach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
 RA Hatch B., Horst K., Roberts K., Sandusky W., Weidman J., Smith H.O.,
 RA Venter J.C.;
 RT "Complete genome sequence of *Treponema pallidum*, the syphilis
 agent";
 RT Spirochaete; -;
 RL Science 281:375-388(1998).
 DR EMBL; AE001220; AAC65422.1; -;
 DR TIGR; TP0434; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 227 AA; 25035 MW; 3FA02711A66B45FE CRC64;
 Query Match 81.2%; Score 82; DB 16; Length 227;
 Best Local Similarity 85.0%; Pred. No. 0.00012;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 EVEDVPKVEPASPAREGGER 20
 |||||
 47 EVEDVPKVEPASPAREGGER 66
 RESULT 8
 095108 PRELIMINARY; PRT; 187 AA.
 AC 095108;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Expressed protein (RD2 protein).
 GN AT2621620.
 OS *Arabidopsis thaliana* (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eustoides II; Brassicales; Brassicaceae; Arabidopsis.
 CX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
 RA Bannstead M.E., Mason T.M., Bowman C.L., Roming C.M., Benito M.-I.,
 RA Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
 RA Fraser C.M., Venter J.C.;
 RL Submitted (F8B-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Hase B.J., Volkovsky N., Town C.D., Troughan M., Alexandrov N.,
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
 RT "Full-length messenger RNA sequences greatly improve genome
 annotation";
 RL Genome Biol. 0:0-0(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Brover V., Troughan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.;
 RT "Full-length cDNA from *Arabidopsis thaliana*";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC007119; AAD23643.2; -;
 DR EMBL; AY087097; AAM64657.1; -;
 DR InterPro; IPR006016; Usp_dom.
 DR Pfam; PF00582; Usp; 1.
 SQ SEQUENCE 187 AA; 20587 MW; BC8146F9BC802B76 CRC64;
 Query Match 49.5%; Score 50; DB 10; Length 187;
 Best Local Similarity 62.5%; Pred. No. 8.9;
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 Oy 5 VPKVEPASPAREGGER 20
 :|||
 21 IPVVEPASPAREGGER 36
 RESULT 9
 094115 PRELIMINARY; PRT; 193 AA.
 AC 094115;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE RD2 protein.
 GN RD2.
 OS *Arabidopsis thaliana* (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eustoides II; Brassicales; Brassicaceae; Arabidopsis.
 CX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Columbia;
 RA Shinzaki K., Yamaguchi-Shinozaki K., Takahashi S.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Columbia;
 RA Yamaguchi-Shinozaki K., Koizumi M., Urao S., Shinzaki K.;
 RT "Molecular cloning and characterization of 9 cDNAs for genes that are
 responsive to desiccation in *Arabidopsis thaliana*: sequence analysis
 of one cDNA clone that encodes a putative transmembrane channel
 protein";
 RL Plant Cell Physiol. 33:217-224(1992).
 DR EMBL; AB039925; BAB63912.1; -;
 DR InterPro; IPR006016; Usp_dom.
 DR Pfam; PF00582; Usp; 1.
 SQ SEQUENCE 193 AA; 21253 MW; EAA5F1D0BFED679 CRC64;

Query Match 49.5%; Score 50; DB 10; Length 193;
 Best Local Similarity 62.5%; Pred. No. 9.2;
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 VKKVEPASERREGG 20
 : | | | | | | | | | |
 DB 21 IPVPEPELERSGGR 36

RESULT 10

Q8WV22 PRELIMINARY; PRT; 256 AA.

AC Q8WV22
 DT 01-MAR-2002 (TRENBLREL. 20, Created)
 DT 01-MAR-2002 (TRENBLREL. 20, Last sequence update)
 DE 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
 OS Similar to RIKEN CDNA 2510027N19 gene.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC018938; AAH18938.1; -
 DR InterPro: IPR000345; Cyt_c_heme_bind.
 DR InterPro: IPR002219; DAG_Pb_bind.
 DR InterPro: IPR001841; ZnF_Ting.
 DR PROSITE: PS00190; CYTOCHROME_C_1.
 DR PROSITE: PS50081; DAG_Pb_BIND_DOM_2; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 SQ SEQUENCE 256 AA; 29724 MW; 3433001005D7EDDF CRC64;

Query Match 48.5%; Score 49; DB 4; Length 256;
 Best Local Similarity 53.3%; Pred. No. 18;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 DVKVEPASERREGG 18
 : | | | | | | | | | |
 DB 228 EIKVDFPEKERSGG 242

RESULT 11

P95090 PRELIMINARY; PRT; 547 AA.

AC P95090
 DT 01-MAY-1997 (TRENBLREL. 03, Created)
 DT 01-MAY-1997 (TRENBLREL. 03, Last sequence update)
 DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
 DE Hypothetical 58.3 kDa protein (Phosphoglucanase).
 GN PGMA OR RV3068C OR MTCY22D7.13 OR MT3153.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinomycetales; Actinomycetales;
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Broch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekla F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagers K., Krogan A., McLean J., Moule S., Murphy J.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sultson J.E., Taylor K., Whitehead S., Barrett B.G.;
 RA "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544 (1998).
 [2]

RP SEQUENCE FROM N.A.

RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Kouri H., Gill J., Mikula A.,
 RA Bishop W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 laboratory strains";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; 283866; CAB06255.1; -
 DR EMBL; AE007132; AAK47488.1; -
 DR TIGR; MT3153; -
 DR Tuberculest; RV3068C; -
 DR InterPro: IPR005841; PG_PBM_mutase.
 DR InterPro: IPR005852; Pglucmut A.
 DR InterPro: IPR005844; PG_PBM_ABAI.
 DR InterPro: IPR005845; PG_PBM_ABAI.
 DR InterPro: IPR005846; PG_PBM_ABAI.
 DR InterPro: IPR005843; PG_PBM_C.
 DR Pfam; PR00408; PGM_PBM_1.
 DR Pfam; PR02878; PGM_PBM_1.
 DR Pfam; PR02879; PGM_PBM_1.
 DR Pfam; PR02880; PGM_PBM_1.
 DR TIGRFAMs; TIGR01132; PGM_1.
 DR PROSITE: PS00710; PGM_PBM_1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 547 AA; 58265 MW; 1825BDE89A9E951 CRC64;

Query Match 47.5%; Score 48; DB 16; Length 547;
 Best Local Similarity 52.6%; Pred. No. 56;
 Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 VEDVKEPASERREGG 20
 : | | | | | | | | | |
 DB 210 VDDLPNVVDIAIRAGVR 228

RESULT 12

Q81BW7 PRELIMINARY; PRT; 2192 AA.

AC Q81BW7
 DT 01-MAR-2003 (TRENBLREL. 23, Created)
 DT 01-MAR-2003 (TRENBLREL. 23, Last sequence update)
 DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
 DE Erythrocyte membrane protein 1 (PEM1).
 GN MAL7P1.56.
 OS Plasmodium falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=36329;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Seeger K., Murphy L., Harris D., Berriman M., Pain A., Hall N.,
 RA Quail M., Barrett B.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL844506; CAD50877.1; -
 SQ SEQUENCE 2192 AA; 248940 MW; 4EAD66FF62A81329 CRC64;

Query Match 47.5%; Score 48; DB 5; Length 2192;
 Best Local Similarity 56.2%; Pred. No. 2.5e+02;
 Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EVEDVKEPASERREGG 16
 : | | | | | | | | | |
 DB 877 EKEAPKVEPAPVKE 892

RESULT 13

Q8CPY0 PRELIMINARY; PRT; 792 AA.

AC Q8CPY0
 DT 01-MAR-2003 (TRENBLREL. 23, Created)
 DT 01-MAR-2003 (TRENBLREL. 23, Last sequence update)

```

DT 01-MAR-2003 (TRENBLrel. 23, last annotation update)
DE Ribonuclease R.
GN SE0565.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12228;
RA Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Yu Y., Qin Z.,
RL Chen Z., Wen Y.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016745; AA004162.1; -.
KW Complete proteome.
SQ SEQUENCE 792 AA; 91110 MW; E83F9C4C98AB7D7F CRC64;

Query Match 47.0%; Score 47.5; DB 16; Length 792;
Best Local Similarity 64.7%; Pred. No. 1e+02;
Matches 11; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 1 EVDVPKVPEPASEREG 17
DB 235 EAEVDPVIEP-SEIEG 250

RESULT 14
Q9D720 PRELIMINARY; PRT; 266 AA.
ID Q9D720.
AC Q9D720.
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DE 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE 2510027N19R1K protein.
GN 2510027N19R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H. A., Ashburner M., Batalov S., Casavant T.,
RA Fletschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiraldi L. M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M. F.,
RA Brownstein M. J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guelincich S., Hill D., Hofmann M., Hume D. A., Kamiya M., Lee N. H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K. H., Weitz C., Whitaker C., Wilming L.,
RA Wyshew-Boris A., Yoshida K., Haegawa Y., Kawaji H., Kontsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK009715; BAB26459.1; -.
DR MGI; MGI:1914961; 2510027N19R1K.
DR InterPro; IPR000345; Cytochrome_bnd.
DR InterPro; IPR002219; DAG_Pe-bind.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS50081; DAG_Pe BIND DOM 2; 1.
SQ SEQUENCE 266 AA; 30708 MW; F5728C530532E03A CRC64;

Query Match 46.5%; Score 47; DB 11; Length 266;
Best Local Similarity 53.3%; Pred. No. 38;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

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QY 4 DVPKVEPASEREG 18
DB 238 DPEVNPKEKEREAG 252

RESULT 15
Q8K2B4 PRELIMINARY; PRT; 280 AA.
ID Q8K2B4.
AC Q8K2B4.
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE RIKEN cDNA 2510027N19 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC031848; AAH31848.1; -.
DR InterPro; IPR000345; Cytochrome_bnd.
DR InterPro; IPR002219; DAG_Pe-bind.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS50081; DAG_Pe BIND DOM 2; 1.
SQ SEQUENCE 280 AA; 32038 MW; CC5BCC949EA269F CRC64;

Query Match 46.5%; Score 47; DB 11; Length 280;
Best Local Similarity 53.3%; Pred. No. 40;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 DVPKVEPASEREG 18
DB 252 DPEVNPKEKEREAG 266

Search completed: August 1, 2003, 18:36:13
Job time : 98 secs

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OX Ictalurid Herpes-like viruses.
OX NCBI_TaxID=10401.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Auburn 1;
RX MEDLINE=92087490; PubMed=1727613;
RA Davison A.J.;
RT "Channel catfish virus: a new type of herpesvirus.";
RL Virology 186:9-14(1992).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M75136; AAA88174.1; -.
DR PIR: G36793; G36793.
DR InterPro: IPR007087; Znf_C2H2.
DR SMART: SM00355; Znf_C2H2; 1.
KW Hypothetical protein.
SO SEQUENCE 1350 AA; 147547 MW; ED4780D2F290FFD CRC64;

Query Match 44.6%; Score 45; DB 1; Length 1350;
Best Local Similarity 50.0%; Pred. No. 70;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Oy 3 EDVPRVPEASREBGER 20
Db :|:|:|:|:|:|
913 KSVKRIEASKEGGER 930

RESULT 5
TRPC_HALVO STANDARD; PRT; 251 AA.
ID _TRPC_HALVO
AC P18304;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Indole-3-glycerol phosphate synthase (EC 4.1.1.48) (IGPS).
GN TRPC.
OS Halobacterium volcanii (Haloferrax volcanii).
OC Archaea; Euryarchaeota; Halobacteriales;
OC Halobacteriaceae; Haloferrax.
OX NCBI_TaxID=2246;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90370836; PubMed=2118654;
RA Lam W.L., Cohen A., Teoulunas D.; Doolittle W.F.;
RT "Genes for tryptophan biosynthesis in the archaebacterium Haloferrax
RT volcanii.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:6614-6618(1990).
CC -1- CATALYTIC ACTIVITY: 1-(2-carboxyphenylamino)-L-deoxy-D-ribose 5-
CC phosphate = 1-(indol-3-yl)glycerol 3-phosphate + CO(2) + H(2)O.
CC -1- PATHWAY: Tryptophan biosynthesis; fourth step.
CC -1- SIMILARITY: BELONGS TO THE TRPC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M36177; AAA72862.1; -.
DR PIR: C36044; C36044.
DR HSSP: O06121; 1A53.
DR HAMAP: MF_00134; -.
DR InterPro: IPR001009; FMN_enzyme.
DR InterPro: IPR001468; IGPS.

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DR Pfam: PF00218; IGPS; 1.
DR Pfam: PD00151; IGPS; 1.
DR PROSITE; PS00614; IGPS; 1.
RW TrypTophan biosynthesis; Lyase; Decarboxylase.
SQ SEQUENCE 251 AA; 26754 MW; 2F2FD9E702B48065 CRC64;

Query Match 43.6%; Score 44; DB 1; Length 251;
Best Local Similarity 56.2%; Pred. NO. 18;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Oy 4 DVPKRVPEASEREQGE 19
Db 11 DVAAILAEARERPGGE 26

RESULT 6
CREM_HUMAN
ID CREM_HUMAN STANDARD; PRT; 332 AA.
AC Q03060; O16114; Q16116; Q9NZ89;
DT 01-JUN-1994 (Rel. 29, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE CAMP responsive element modulator.
GN CREM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC TISSUE=Placenta;
RX MEDLINE=93096608; PubMed=1461747;
RA "Meyler T.E., Habener J.P.;
RT "Cyclic AMP response element binding protein CREB and modulator
RT protein CREM are products of distinct genes.";
RL Nucleic Acids Res. 20:6106-6106(1992).
RN [2]
RX SEQUENCE FROM N.A. (ISOFORM BETA).
RX MEDLINE=94128610; PubMed=7916662;
RA "Maquillier D., Foulkes N.S., Mattei M.-G., Saesone-Corsi P.;
RT "Human CREM gene: evolutionary conservation, chromosomal localization,
RT and inducibility of the transcript.";
RL Cell Growth Differ. 4:931-937(1993).
RN [3]
RX SEQUENCE OF 1-232 FROM N.A.
RP Vouk K., Lallit B., Scherer S.W., Saesone-Corsi P., Debeljak N.,
RA Komel R., Rosman D.;
RT "Searching for mutations in the human CAMP responsive element
RT modulator (CREM) gene.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE), A
CC SEQUENCE PRESENT IN MANY VIRAL AND CELLULAR PROMOTERS. CREM ALPHA,
CC BETA, AND GAMMA ISOFORMS ARE ANTAGONISTS OF THE CAMP
CC TRANSCRIPTIONAL RESPONSE, WHILE THE DELTA ISOFORM IS AN ACTIVATOR.
CC -1- SUBUNIT: Binds DNA as a dimer (by similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=Beta;
CC IsoId=Q03060-1; Sequence=Displayed;
CC Name=Alpha;
CC IsoId=Q03060-2; Sequence=VSP_000599, VSP_000600, VSP_000601;
CC Name=Gamma;
CC IsoId=Q03060-4; Sequence=Not described;
CC Name=Delta;
CC IsoId=Q03060-3; Sequence=Not described;
CC -1- PTM: STIMULATED BY PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to the bZIP family.
CC -----
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CC EMBL: Z51519; CAA78858.1; -
 CC EMBL: S68134; AAC60617.2; -
 CC EMBL: S68271; AAC60616.2; ALT_SEQ.
 CC EMBL: AF213899; AAF68266.2; -
 CC EMBL: AF213158; AAF68266.2; JOINED.
 CC EMBL: AF213897; AAF68266.2; JOINED.
 CC EMBL: AF213898; AAF68266.2; JOINED.
 CC TRANSFAC; T01803; -
 CC Genew; HGNC:2352; CREM.
 CC MIM; 123812; -
 CC GO; GO:0005634; C:nucleus; TAS.
 CC GO; GO:0007165; P:signal transduction; TAS.
 CC InterPro; IPR001630; Leuzip_CREB.
 CC InterPro; IPR003102; PKID.
 CC InterPro; IPR004827; TF_bZIP.
 CC Pfam; PF00170; bZIP; 2.
 CC Pfam; PF02173; PKID; 2.
 CC PRINTS; PR00041; LEUZIPRCREB.
 CC SMART; SM00338; BRLZ; 1.
 CC PROSITE; PS0217; BZIP; 1.
 CC PROSITE; PS00036; BZIP_BASIC; 1.
 CC Transcription regulation; DNA-binding; Repressor; Phosphorylation;
 CC Nuclear protein; Alternative splicing.
 CC DNA BIND 275 BASIC MOTIF (BY SIMILARITY).
 CC DOMAIN 302 LEUCINE-ZIPPER (BY SIMILARITY).
 CC VARSPLIC 42 Missing (in isoform Alpha).
 CC VARSPLIC 170 Missing (in isoform Alpha).
 CC VARSPLIC 232 Missing (in isoform Alpha).
 CC VARSPLIC 233 A -> T (in isoform Alpha).
 CC FT CONFLICT 33 N -> I (IN REF. 2).
 CC FT CONFLICT 39 A -> R (IN REF. 1).
 CC FT CONFLICT 41 VSVAG -> CSELR (IN REF. 2).
 CC FT CONFLICT 332 D -> DY (IN REF. 2).
 CC FT SEQUENCE 332 AA; 35531 MW; 1D014C2EA416D72A CRC64;
 SQ

Query Match 43.6%; Score 44; DB 1; Length 332;
 Best Local Similarity 52.9%; Pred. No. 24;
 Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 EYEDVPKXVEPASEREG 17
 DB 131 DVGVPKIEERSEERG 147

RESULT 7

CREM CANFA
 ID CREM_CANFA STANDARD; PRT; 344 AA.
 AC P79145;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE CAMP responsive element modulator.
 GN CREM.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 CC NCBI_Taxid:9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thyroid;
 RX MEDLINE=97410117; PubMed=9266832;
 RA Uyteyereproc N., Mot F.;
 RT "Dog CREM transcription factors: cloning, tissue distribution, and
 identification of new isoforms."
 RL Biochem. Biophys. Res. Commun. 237:74-78(1997).
 CC -!- FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE), A
 SEQUENCE PRESENT IN MANY VIRAL AND CELLULAR PROMOTERS. CREM ALPHA,

CC BETA, AND GAMMA ISOFORMS ARE ANTAGONISTS OF THE CAMP
 CC TRANSCRIPTIONAL RESPONSE, WHILE THE DELTA ISOFORM IS AN ACTIVATOR.
 CC -!- SUBUNIT: Binds DNA as a dimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=Delta;
 CC IsoId=P79145-1; Sequence=Displayed;
 CC Name=Alpha;
 CC IsoId=P79145-2; Sequence=Not described;
 CC Name=Beta;
 CC IsoId=P79145-3; Sequence=Not described;
 CC Name=Gamma;
 CC IsoId=P79145-4; Sequence=Not described;
 CC -!- PTM: STIMULATED BY PHOSPHORYLATION (BY SIMILARITY).
 CC -!- SIMILARITY: Belongs to the bZIP family.

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CC EMBL: X99115; CAA67563.1; -
 CC PIR; JCS601; JCS601.
 CC InterPro; IPR001630; Leuzip_CREB.
 CC InterPro; IPR003102; PKID.
 CC InterPro; IPR004827; TF_bZIP.
 CC Pfam; PF00170; bZIP; 1.
 CC Pfam; PF02173; PKID; 1.
 CC PRINTS; PR00041; LEUZIPRCREB.
 CC SMART; SM00338; BRLZ; 1.
 CC PROSITE; PS0217; BZIP; 1.
 CC PROSITE; PS00036; BZIP_BASIC; 1.
 CC Transcription regulation; DNA-binding; Activator; Repressor;
 CC Phosphorylation; Nuclear protein; Alternative splicing.
 CC DNA BIND 287 BASIC MOTIF (BY SIMILARITY).
 CC FT DOMAIN 314 335 LEUCINE-ZIPPER (BY SIMILARITY).
 CC FT SEQUENCE 344 AA; 36915 MW; 7CF50FE32322918 CRC64;
 SQ

Query Match 43.6%; Score 44; DB 1; Length 344;
 Best Local Similarity 52.9%; Pred. No. 24;
 Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 EYEDVPKXVEPASEREG 17
 DB 131 DVGVPKIEERSEERG 147

RESULT 8

AMPH CHICK
 ID AMPH_CHICK STANDARD; PRT; 682 AA.
 AC P50478;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Amphiphsin.
 GN AMPH.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 CC NCBI_Taxid=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Tetra-hybrid; TISSUE=Forebrain;
 RX MEDLINE=92331604; PubMed=1628617;
 RA Lichte B., Voh R.W., Meyer H.E., Kilmann M.W.;
 RT "Amphiphsin, a novel protein associated with synaptic vesicles."
 RL EMBO J. 11:2521-2530(1992).
 CC -!- FUNCTION: MAY PARTICIPATE IN MECHANISMS OF REGULATED EXOCYTOSIS IN

CC SYNAPSES AND CERTAIN ENDOCRINE CELL TYPES. MAY CONTROL THE
 CC PROPERTIES OF THE MEMBRANE ASSOCIATED CYTOSKELETON.
 CC SUBCELLULAR LOCATION: ASSOCIATED WITH THE CYTOPLASMIC SURFACE OF
 CC SYNAPTIC VESICLES.
 CC TISSUE SPECIFICITY: IS ABUNDANT IN THE FOREBRAIN AND CEREBELLUM.
 CC IT IS ALSO FOUND IN THE ADRENAL GLAND, ANTERIOR AND POSTERIOR
 CC PITUITARY.
 CC SIMILARITY: Contains 1 BAR domain.
 CC SIMILARITY: Contains 1 SH3 domain.
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 CC -----
 CC EMBL: X60422; CAA42953.1; -
 CC PIR: S22700; S22700.
 CC InterPro: IPR003005; Amphiphysin.
 CC InterPro: IPR003017; Amphiphysin_1.
 CC InterPro: IPR006632; BAR.
 CC InterPro: IPR004148; BAR_dom.
 CC InterPro: IPR001452; SH3.
 CC Pfam: PF03114; BAR; 1.
 CC Pfam: PF00018; SH3; 1.
 CC PRINTS: PR01251; AMPHIPHYSIN.
 CC PRINTS: PR00452; SH3DOMAIN.
 CC ProDom: PD003208; Amphiphysin_1.
 CC ProDom: PD000066; SH3; 1.
 CC SMART: SM00721; BAR; 1.
 CC PROSITE: PS00326; SH3; 1.
 CC PROSITE: PS50002; SH3; 1.
 CC Cytokeleton; SH3 domain; Coiled coil.
 CC KW DOMAIN 10 84 COILED COIL (POTENTIAL).
 CC FT DOMAIN 144 191 COILED COIL (POTENTIAL).
 CC FT DOMAIN 609 682 SH3.
 CC SQ SEQUENCE 682 AA; 75205 MW; 61617P494F38EB20 CRC64;
 CC
 CC Query Match 43.6%; Score 44; DB 1; Length 682;
 CC Best Local Similarity 57.1%; Pred. No. 49;
 CC Matches 12; Conservative 2; Mismatches 5; Indels 2; Gaps 2;
 CC
 CC QY 1 EVEDVPKVV-EPASREG-GE 19
 CC DB 529 KVSISPVVIRPANSNEGE 549
 CC
 CC RESULT 9
 CC SYV_METH STANDARD; PRT; 877 AA.
 CC AC O2661.
 CC DT 15-JUL-1998 (Rel. 36, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE Valyl-tRNA synthetase (EC 6.1.1.9) (Valine--tRNA ligase) (ValRS).
 CC GN VALS OR MTH767.
 CC OS Methanobacterium thermoautotrophicum.
 CC OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriales;
 CC OC Methanobacteriaceae; Methanothermobacter.
 CC OX NCBI_TaxID=187420;
 CC (1)
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=Delta H;
 CC RX MEDLINE=98037514; PubMed=9371463;
 CC RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
 CC Aldegrete T., Bashirizadeh R., Blakey D., Cook R., Gilbert K.,
 CC Harrison D., Hoang L., Keagle P., Lum W., Pothier B., Qiu D.,
 CC Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 CC Jiwani N., Canuso A., Bush D., Saefer H., Patwell J.D., Prakhakar S.,
 CC McDougall S., Shimer G., Goyal A., Plectovski S., Church G.M.,
 CC Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;

RT "Complete genome sequence of Methanobacterium thermoautotrophicum
 RT deltaH: functional analysis and comparative genomics.";
 RT J. Bacteriol. 179:7135-7155 (1997).
 CC -1- CATALYTIC ACTIVITY: ATP + L-valine + tRNA(Val) = AMP + diphosphate
 CC + L-valyl-tRNA(Val).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AE000855; AAB85270.1; -
 CC HSSP: P96142; IGX.
 CC InterPro: IPR002300; tRNA-synt 1a.
 CC InterPro: IPR001412; tRNA-synt 1.
 CC InterPro: IPR002303; tRNA-synt_val.
 CC Pfam: PF00133; tRNA-synt 1; 1.
 CC PRINTS: PR00386; TRNASYNTHAL.
 CC TIGRFAMs: TIGR00422; valS; 1.
 CC PROSITE: PS00178; AA tRNA_LIGASE_I; 1.
 CC KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 CC Complete proteome.
 CC FT SITE 46 56 "HIGH" REGION.
 CC FT SITE 529 533 "RMSK" REGION.
 CC FT BINDING 532 532 ATP (BY SIMILARITY).
 CC SQ SEQUENCE 877 AA; 100946 MW; B939720D6DF8F0DB CRC64;
 CC
 CC Query Match 43.6%; Score 44; DB 1; Length 877;
 CC Best Local Similarity 46.7%; Pred. No. 64;
 CC Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 CC
 CC QY 3 EDVPRVVEPASEREG 17
 CC DB 709 EHPIEIVDPBIRSG 723
 CC
 CC RESULT 10
 CC PCH7_HUMAN STANDARD; PRT; 1069 AA.
 CC AC O60245; O60246; O60247;
 CC DT 28-FEB-2003 (Rel. 41, Created)
 CC DT 28-FEB-2003 (Rel. 41, Last sequence update)
 CC DT 15-SEP-2003 (Rel. 41, Last annotation update)
 CC DE Protocadherin 7 precursor (Brain-heart protocadherin) (BH-Pcdh).
 CC GN PCDH7 OR BHPCDH.
 CC OS Homo sapiens (Human).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CC OX NCBI_TaxID=9606;
 CC (1)
 CC RP SEQUENCE FROM N.A. (ISOFORMS A; B AND C).
 CC RX MEDLINE=98277460; PubMed=9615233;
 CC RA Yoshida K., Yoshitomo-nakagawa K., Seki N., Sasaki M., Sugano S.;
 CC "Cloning, expression analysis, and chromosomal localization of
 CC BH-protocadherin (PCDH7), a novel member of the cadherin
 CC superfamily";
 CC RL Genomics 49:458-461 (1998).
 CC CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=A; Synonyms=BH-Pcdh-a;
 CC Name=B; Synonyms=BH-Pcdh-b;
 CC Name=C; Synonyms=BH-Pcdh-c;
 CC Name=D; Synonyms=BH-Pcdh-d;
 CC Name=E; Synonyms=BH-Pcdh-e;
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 CC Name=CF; Synonyms=BH-Pcdh-CF;
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 CC Name=CH; Synonyms=BH-Pcdh-CH;
 CC Name=CI; Synonyms=BH-Pcdh-CI;
 CC Name=CJ; Synonyms=BH-Pcdh-CJ;
 CC Name=CK; Synonyms=BH-Pcdh-CK;
 CC Name=CL; Synonyms=BH-Pcdh-CL;
 CC Name=CM; Synonyms=BH-Pcdh-CM;
 CC Name=CN; Synonyms=BH-Pcdh-CN;
 CC Name=CO; Synonyms=BH-Pcdh-CO;
 CC Name=CP; Synonyms=BH-Pcdh-CP;
 CC Name=CQ; Synonyms=BH-Pcdh-CQ;
 CC Name=CR; Synonyms=BH-Pcdh-CR;
 CC Name=CS; Synonyms=BH-Pcdh-CS;
 CC Name=CT; Synonyms=BH-Pcdh-CT;
 CC Name=CU; Synonyms=BH-Pcdh-CU;
 CC Name=CV; Synonyms=BH-Pcdh-CV;
 CC Name=CW; Synonyms=BH-Pcdh-CW;
 CC Name=CX; Synonyms=BH-Pcdh-CX;
 CC Name=CY; Synonyms=BH-Pcdh-CY;
 CC Name=CA; Synonyms=BH-Pcdh-CA;
 CC Name=CB; Synonyms=BH-Pcdh-CB;
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 CC Name=CD; Synonyms=BH-Pcdh-CD;
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 CC Name=CF; Synonyms=BH-Pcdh-CF;
 CC Name=CG; Synonyms=BH-Pcdh-CG;
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 CC Name=CI; Synonyms=BH-Pcdh-CI;
 CC Name=CJ; Synonyms=BH-Pcdh-CJ;
 CC Name=CK; Synonyms=BH-Pcdh-CK;
 CC Name=CL; Synonyms=BH-Pcdh-CL;
 CC Name=CM; Synonyms=BH-Pcdh-CM;
 CC Name=CN; Synonyms=BH-Pcdh-CN;
 CC Name=CO; Synonyms=BH-Pcdh-CO;
 CC Name=CP; Synonyms=BH-Pcdh-CP;
 CC Name=CQ; Synonyms=BH-Pcdh-CQ;
 CC Name=CR; Synonyms=BH-Pcdh-CR;
 CC Name=CS; Synonyms=BH-Pcdh-CS;
 CC Name=CT; Synonyms=BH-Pcdh-CT;
 CC Name=CU; Synonyms=BH-Pcdh-CU;
 CC Name=CV; Synonyms=BH-Pcdh-CV;
 CC Name=CW; Synonyms=BH-Pcdh-CW;
 CC Name=CX; Synonyms=BH-Pcdh-CX;
 CC Name=CY; Synonyms=BH-Pcdh-CY;
 CC Name=CA; Synonyms=BH-Pcdh-CA;
 CC Name=CB; Synonyms=BH-Pcdh-CB;
 CC Name=CC; Synonyms=BH-Pcdh-CC;
 CC Name=CD; Synonyms=BH-Pcdh-CD;
 CC Name=CE; Synonyms=BH-Pcdh-CE;
 CC Name=CF; Synonyms=BH-Pcdh-CF;
 CC Name=CG; Synonyms=BH-Pcdh-CG;
 CC Name=CH; Synonyms=BH-Pcdh-CH;
 CC Name=CI; Synonyms=BH-Pcdh-CI;
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 CC Name=CL; Synonyms=BH-Pcdh-CL;
 CC Name=CM; Synonyms=BH-Pcdh-CM;
 CC Name=CN; Synonyms=BH-Pcdh-CN;
 CC Name=CO; Synonyms=BH-Pcdh-CO;
 CC Name=CP; Synonyms=BH-Pcdh-CP;
 CC Name=CQ; Synonyms=BH-Pcdh-CQ;
 CC Name=CR; Synonyms=BH-Pcdh-CR;
 CC Name=CS; Synonyms=BH-Pcdh-CS;
 CC Name=CT; Synonyms=BH-Pcdh-CT;
 CC Name=CU; Synonyms=BH-Pcdh-CU;
 CC Name=CV; Synonyms=BH-Pcdh-CV;
 CC Name=CW; Synonyms=BH-Pcdh-CW;
 CC Name=CX; Synonyms=BH-Pcdh-CX;
 CC Name=CY; Synonyms=BH-Pcdh-CY;
 CC Name=CA; Synonyms=BH-Pcdh-CA;
 CC Name=CB; Synonyms=BH-Pcdh-CB;
 CC Name=CC; Synonyms=BH-Pcdh-CC;
 CC Name=CD; Synonyms=BH-Pcdh-CD;
 CC Name=CE; Synonyms=BH-Pcdh-CE;
 CC Name=CF; Synonyms=BH-Pcdh-CF;
 CC Name=CG; Synonyms=BH-Pcdh-CG;
 CC Name=CH; Synonyms=BH-Pcdh-CH;
 CC Name=CI; Synonyms=BH-Pcdh-CI;
 CC Name=CJ; Synonyms=BH-Pcdh-CJ;
 CC Name=CK; Synonyms=BH-Pcdh-CK;
 CC Name=CL; Synonyms=BH-Pcdh-CL;
 CC Name=CM; Synonyms=BH-Pcdh-CM;
 CC Name=CN; Synonyms=BH-Pcdh-CN;
 CC Name=CO; Synonyms=BH-Pcdh-CO;
 CC Name=CP; Synonyms=BH-Pcdh-CP;
 CC Name=CQ; Synonyms=BH-Pcdh-CQ;
 CC Name=CR; Synonyms=BH-Pcdh-CR;
 CC Name=CS; Synonyms=BH-Pcdh-CS;
 CC Name=CT; Synonyms=BH-Pcdh-CT;
 CC Name=CU; Synonyms=BH-Pcdh-CU;
 CC Name=CV; Synonyms=BH-Pcdh-CV;
 CC Name=CW; Synonyms=BH-Pcdh-CW;
 CC Name=CX; Synonyms=BH-Pcdh-CX;
 CC Name=CY; Synonyms=BH-Pcdh-CY;
 CC Name=CA; Synonyms=BH-Pcdh-CA;
 CC Name=CB; Synonyms=BH-Pcdh-CB;
 CC Name=CC; Synonyms=BH-Pcdh-CC;
 CC Name=CD; Synonyms=BH-Pcdh-CD;
 CC Name=CE; Synonyms=BH-Pcdh-CE;
 CC Name=CF; Synonyms=BH-Pcdh-CF;
 CC Name=CG; Synonyms=BH-Pcdh-CG;
 CC Name=CH; Synonyms=BH-Pcdh-CH;
 CC Name=CI; Synonyms=BH-Pcdh-CI;
 CC Name=CJ; Synonyms=BH-Pcdh-CJ;
 CC Name=CK; Synonyms=BH-Pcdh-CK;
 CC Name=CL; Synonyms=BH-Pcdh-CL;
 CC Name=CM; Synonyms=BH-Pcdh-CM;
 CC Name=CN; Synonyms=BH-Pcdh-CN;
 CC Name=CO; Synonyms=BH-Pcdh-CO;
 CC Name=CP; Synonyms=BH-Pcdh-CP;
 CC Name=CQ; Synonyms=BH-Pcdh-CQ;
 CC Name=CR; Synonyms=BH-Pcdh-CR;
 CC Name=CS; Synonyms=BH-Pcdh-CS;
 CC Name=CT; Synonyms=BH-Pcdh-CT;
 CC Name=CU; Synonyms=BH-Pcdh-CU;
 CC Name=CV; Synonyms=BH-Pcdh-CV;
 CC Name=CW; Synonyms=BH-Pcdh-CW;
 CC Name=CX; Synonyms=BH-Pcdh-CX;
 CC Name=CY; Synonyms=BH-Pcdh-CY;
 CC Name=CA; Synonyms=BH-Pcdh-CA;
 CC Name=CB; Synonyms=BH-Pcdh-CB;
 CC Name=CC; Synonyms=BH-Pcdh-CC;
 CC Name=CD; Synonyms=BH-Pcdh-CD;
 CC Name=CE; Synonyms=BH-Pcdh-CE;
 CC Name=CF; Synonyms=BH-Pcdh-CF;
 CC Name=CG; Synonyms=BH-Pcdh-CG;
 CC Name=CH; Synonyms=BH-Pcdh-CH;
 CC Name=CI; Synonyms=BH-Pcdh-CI;
 CC Name=CJ; Synonyms=BH-Pcdh-CJ;
 CC Name=CK; Synonyms=BH-Pcdh-CK;
 CC Name=CL; Synonyms=BH-Pcdh-CL;
 CC Name=CM; Synonyms=BH-Pcdh-CM;
 CC Name=CN; Synonyms=BH-Pcdh-CN;
 CC Name=CO; Synonyms=BH-Pcdh-CO;
 CC Name=CP; Synonyms=BH-Pcdh-CP;
 CC Name=CQ; Synonyms=BH-Pcdh-CQ;
 CC Name=CR; Synonyms=BH-Pcdh-CR;
 CC Name=CS; Synonyms=BH-Pcdh-CS;
 CC Name=CT; Synonyms=BH

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE DNA (cytosine-5-methyltransferase 1 (BC 2.1.1.37) (Dnmt1) (DNA methyltransferase Ggal) (DNA Mase Ggal) (MCMT) (M.ggal).

DE DNMT1 OR DNMT OR AIM.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OX NCBI_TaxID=9031;

XX [1]

XX SEQUENCE FROM N.A.

XX MEDLINE=96172572; PubMed=8586618;

XX Tajima S., Tsuda H., Wakabayashi N., Aaseo A., Mizuno S.,

XX Nishimori K.,

XX "Isolation and expression of a chicken DNA methyltransferase cDNA,"

XX J. Biochem. 117:1050-1057(1995).

XX [2]

XX INTERACTION WITH PCNA, AND MUTAGENESIS OF VAL-190.

XX MEDLINE=97451025; PubMed=9302295;

XX Chuang L.S.-H., Ian H.-I., Koh T.-W., Ng H.-H., Xu G., Li B.F.L.;

XX "Human DNA-(cytosine-5) methyltransferase-PCNA complex as a target for

XX p21WAF1,"

XX Science 277:1996-2000(1997).

XX -1- FUNCTION: Methylates CpG residues. Preferentially methylates

XX hemimethylated DNA. It is responsible for maintaining methylation

XX patterns established in development (By similarity). Mediates

XX transcriptional repression by direct binding to HDAC2 (By

XX similarity).

XX -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA = S-adenosyl-L-

XX homocysteine + DNA containing 5-methylcytosine.

XX -1- SUBUNIT: Interacts with PCNA.

XX -1- SUBCELLULAR LOCATION: Nuclear (By similarity).

XX -1- TISSUE SPECIFICITY: Testis and lung.

XX -1- SIMILARITY: BELONGS TO THE C5-METHYLTRANSFERASE FAMILY.

XX -1- SIMILARITY: Contains 2 BAH domains.

XX -1- SIMILARITY: Contains 1 CXXC-type zinc finger.

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CC EMBL; DA3920; BAA07867.1; -

DR PIR; JC4172; JC4172.

DR REBASE; 3020; M.G9A1.

DR InterPro; IPR001025; BAH.

DR InterPro; IPR001525; C5_DNA_meth.

DR InterPro; IPR002857; Znf_CXXC.

DR Pfam; PF01426; BAH; 2.

DR Pfam; PF00145; DNA_methylase; 1.

DR Pfam; PF02008; zf-CXXC; 1.

DR PRINTS; PR00105; CSMETTRFRASE.

DR SMART; SM00439; BAH; 2.

DR TIGRFAMs; TIGR00675; dcm; 1.

DR PROSITE; PS00094; C5_MTASE_1; 1.

DR PROSITE; PS00095; C5_MTASE_2; 1.

KW DNAtransferase; Methyltransferase; Transcription regulation; Repressor;

KW DNA-binding; zinc-finger; zinc; Metal-binding; Nuclear protein;

KW Repeat; Phosphorylation.

KW Repeat; Phosphorylation.

FT DOMAIN 182 194

FT ZN FING 557 603

FT CXXC-TYPE 667 791

FT BAH 1.

FT DOMAIN 877 1011

FT DOMAIN 1020 1034

FT DOMAIN 129 149

FT POLY-SER.

FT POLY-GLU.

FT PHOSPHORYLATION (BY SIMILARITY).

FT MOD RES 217 227

FT ACT SITE 1141 1141

FT BY SIMILARITY.

FT MUTAGEN 190 190 V->H: NO LOSS OF INTERACTION WITH PCNA.
SQ SEQUENCE 1537 AA; 172906 MW; FB7E0B2CD10EA17E CRC64;
Query Match 43.6%; Score 44; DB 1; Length 1537;
Best Local Similarity 46.7%; Pred. No. 11e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
OY 3 EDVKEVPEASEREG 17
:::|||||:
Db 816 KEIPKVAEPLEBGGD 830
RESULT 12
APC_RAT STANDARD; PRT; 2842 AA.
AC P70378;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Adenomatous polyposis coli protein (APC protein).
GN APC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Fischer 344/N; TISSUE=Brain;
RA MEDLINE=96116966; PubMed=8563176;
RA Toyota M., Ushijima T., Kakiuchi H., Watanabe M., Imai K., Yachi A.,
RA Sugimura T., Nago M.;
RT "cDNA cloning of the rat APC gene and assignment to chromosome 18.";
RL Mamm. Genome 6:746-748(1995).
RN [2]
RP MUTAGENESIS.
RX STRAIN=Sprague-Dawley, and Fischer 344/N;
RA MEDLINE=95148647; PubMed=7846077;
RA Kakiuchi H., Watanabe M., Ushijima T., Toyota M., Imai K.,
RA Weisburger J.H., Sugimura T., Nago M.;
RT "Specific 5'-GCCG-3'--5'-GCA-3' mutation of the APC gene in rat colon
tumors induced by 2-amino-1-methyl-6-phenylimidazo(4,5-b)pyridine.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:910-914(1995).
CC -1- FUNCTION: Tumor suppressor. Promotes rapid degradation of CTNNB1
and participates in Wnt signaling. APC activity is correlated with
its phosphorylation state (By similarity).
CC -1- SUBUNIT: Forms homooligomers. Associates with catenins. Binds
axin (By similarity).
CC -1- PTM: PHOSPHORYLATED BY GSK-3B (BY SIMILARITY).
CC -1- SIMILARITY: Contains 7 ARM repeats.
CC -----
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CC -----
DR EMBL; D38629; BAA07609.1; -;
DR HSSP; Q02248; 3BCT.
DR InterPro; IPR000225; Armadillo.
DR Pfam; PF00514; Armadillo_seg; 4.
DR SMART; SMO0185; ARM; 5.
DR PROSITE; PS00766; ARM_REPEAT; 1.
KW Wnt signaling pathway; Anti-oncogene; Phosphorylation; Coiled coil;
Repeat.
KW DOMAIN 1 728 LEU-RICH.
FT DOMAIN 1 62 COILED COIL (POTENTIAL).
FT DOMAIN 125 260 COILED COIL (POTENTIAL).
FT REPEAT 451 493 ARM 1.
FT REPEAT 503 545 ARM 2.
FT REPEAT 546 589 ARM 3.
FT REPEAT 590 636 ARM 4.

FT REPEAT 637 681 ARM 5.
FT REPEAT 682 723 ARM 6.
FT REPEAT 724 765 ARM 7.
FT DOMAIN 739 2831 SER-RICH.
FT DOMAIN 1130 1155 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 1556 1575 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 1864 1891 HIGHLY CHARGED.
FT MUTAGEN 523 523 C->R: IN AN IO-INDUCED COLON TUMOR.
SQ SEQUENCE 2842 AA; 310530 MW; 3CB82EA8A34E8F47 CRC64;
Query Match 43.1%; Score 43.5; DB 1; Length 2842;
Best Local Similarity 55.6%; Pred. No. 2.5e+02;
Matches 10; Conservative 3; Mismatches 4; Indels 1; Gaps 1;
OY 4 DVPEVPEASE-REGGER 20
:::|||||:
Db 1450 EVPEKTVPALEKREGPK 1467
RESULT 13
CREM_MOUSE STANDARD; PRT; 341 AA.
AC P27693; P27698;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE CAMP responsive element modulator.
GN CREM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA; BETA AND GAMMA).
RX MEDLINE=91145994; PubMed=1847666;
RA Foulkes N.S., Borrelli E., Sassone-Corsi P.;
RT "CREM gene: use of alternative DNA-binding domains generates multiple
antagonists of CAMP-induced transcription.";
RL Cell 64:739-749(1991).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM TAU).
RX MEDLINE=92119338; PubMed=1370576;
RA Foulkes N.S., Mellstrom B., Benuiglio E., Sassone-Corsi P.;
RT "Developmental switch of CREM function during spermatogenesis: from
antagonist to activator.";
RL Nature 355:80-84(1992).
CC -1- FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE), A
SEQUENCE PRESENT IN MANY VIRAL AND CELLULAR PROMOTERS. ISOFORMS
ALPHA, BETA, AND GAMMA ARE ANTAGONISTS OF THE CAMP TRANSCRIPTIONAL
RESPONSE. WHILE ISOFORM TAU IS AN ACTIVATOR.
CC -1- SUBUNIT: Binds DNA as a dimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named Isoforms=4;
Name=Tau;
Name=Alpha;
IsoId=P27699-1; Sequence=Displayed;
Name=beta;
IsoId=P27699-2; Sequence=VSP_000602, VSP_000603, VSP_000604,
VSP_000607;
Name=gamma;
IsoId=P27699-3; Sequence=VSP_000602, VSP_000603, VSP_000604;
Name=delta;
IsoId=P27699-4; Sequence=VSP_000602, VSP_000605, VSP_000606;
CC -1- DEVELOPMENTAL STAGE: IN PREMITOTIC GERM CELLS, EXPRESSED AT LOW
AMOUNTS IN THE ANTAGONIST FORM. SUBSEQUENTLY, DURING
SPERMATOGENESIS, THE ISOFORM TAU (ACTIVATOR) IS GENERATED
EXCLUSIVELY AND IN EXTREMELY HIGH AMOUNT.
CC -1- PTM: STIMULATED BY PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to the bZIP family.
CC -----
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CC -----
DR EMBL; M60285; AAA17495.1; -
DR EMBL; M60285; AAA17496.1; -
DR PIR; A37944; A37944.
DR PIR; B37944; B37944.
DR PIR; C37944; C37944.
DR PIR; S20827; S20827.
DR TRANSFAC; T01309; -
DR TRANSFAC; T01314; -
DR TRANSFAC; T01315; -
DR TRANSFAC; T01316; -
DR TRANSFAC; T01602; -
DR TRANSFAC; T02108; -
DR TRANSFAC; T02109; -
DR MGD; MGI:88495; Crem.
DR GO; GO:0005667; C:transcription factor complex; IDA.
DR InterPro; IPR001630; leuzip_CREB.
DR InterPro; IPR003102; PKID.
DR InterPro; IPR004827; TF_BZIP.
DR Pfam; PF00170; bzip; 1.
DR Pfam; PF02173; PKID; 1.
DR PRINTS; PR00041; LEUZIPPCREB.
DR SMART; SM00338; BRLZ; 1.
DR PROSITE; PS50217; BZIP; 1.
DR PROSITE; PS00036; BZIP_BASIC; 1.
KW Transcription regulation; DNA-binding; Activator; Repressor;
KW Phosphorylation; Nuclear protein; Alternative splicing.
FT DOMAIN 311 332 LEUCINE-ZIPPER.
FT VARSPLIC 39 87 Missing (in isoform Alpha, isoform Beta
and isoform Gamma).
FT FT /FTid=VSP 000602.
FT VARSPLIC 167 229 Missing (in isoform Alpha and isoform
Beta).
FT FT /FTid=VSP 000603.
FT VARSPLIC 230 230 D -> N (in isoform Alpha and isoform
Beta).
FT FT /FTid=VSP 000604.
FT VARSPLIC 167 241 Missing (in isoform Gamma).
FT FT /FTid=VSP 000605.
FT VARSPLIC 242 242 A -> T (in isoform Gamma).
FT FT /FTid=VSP 000606.
FT VARSPLIC 298 341 KECRRKKKEIVKLESRVAVLEVONKGLIEELTKDICS
KTD -> RECCRRKKKEIVKLESRVAVLEVONKGLIEELTKDICS
KW Phosphorylation; Nuclear protein; Alternative splicing.
FT FT /FTid=VSP 000607.
FT VARSPLIC 341 AA; 36576 MW; DC8F8C8AD3D219F CRC64;
SQ SEQUENCE 341 AA; 36576 MW; DC8F8C8AD3D219F CRC64;
Query Match 42.6%; Score 43; DB 1; Length 341;
Best Local Similarity 47.1%; Pred. No. 34;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
Oy 1 EVEDVPKVVPEASEREG 17
Db 128 DVGPIPKIEKSEBEG 144

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CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CC NCBI_TaxId=10116;
CC [1]
CC SEQUENCE FROM N.A.
CC TISSUE=Testis;
CC MEDLINE=93096608; PubMed=1461747;
CC Meyer T.E., Habener J.F.;
CC "Cyclic AMP response element binding protein CREB and modulator
CC protein CREM are products of distinct genes.";
CC Nucleic Acids Res. 20:6106-6106(1992).
CC -1- FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE), A
CC SEQUENCE PRESENT IN MANY VIRAL AND CELLULAR PROMOTERS. CREM ALPHA,
CC BETA, AND GAMMA ISOFORMS ARE ANTAGONISTS OF THE CAMP
CC TRANSCRIPTIONAL RESPONSE, WHILE THE DELTA ISOFORM IS AN ACTIVATOR.
CC -1- SUBUNIT: Binds DNA as a dimer (by similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=Delta;
CC IsoId=Q03061-1; Sequence=Displayed;
CC Name=Alpha;
CC IsoId=Q03061-2; Sequence=Not described;
CC Name=Beta;
CC IsoId=Q03061-3; Sequence=Not described;
CC Name=Gamma;
CC IsoId=Q03061-4; Sequence=Not described;
CC -1- PTM: STIMULATED BY PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to the bzip family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; Z15158; CAA78857.1; -
CC DR PIR; S26686; S26686.
CC DR HSSP; P03069; 2DGC.
CC DR TRANSFAC; T01919; -
CC DR InterPro; IPR001630; Leuzip_CREB.
CC DR InterPro; IPR003102; PKID.
CC DR InterPro; IPR004827; TF_BZIP.
CC Pfam; PF00170; bzip; 1.
CC Pfam; PF02173; PKID; 1.
CC PRINTS; PR00041; LEUZIPPCREB.
CC SMART; SM00338; BRLZ; 1.
CC PROSITE; PS50217; BZIP; 1.
CC PROSITE; PS00036; BZIP_BASIC; 1.
KW Transcription regulation; DNA-binding; Activator; Repressor;
KW Phosphorylation; Nuclear protein; Alternative splicing.
FT DNA BIND 284 305 BASIC MOTIF (BY SIMILARITY).
FT DOMAIN 311 332 LEUCINE-ZIPPER (BY SIMILARITY).
FT FT /FTid=VSP 000607.
FT VARSPLIC 341 AA; 36628 MW; IDE75214670125F CRC64;
SQ SEQUENCE 341 AA; 36628 MW; IDE75214670125F CRC64;
Query Match 42.6%; Score 43; DB 1; Length 341;
Best Local Similarity 47.1%; Pred. No. 34;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
Oy 1 EVEDVPKVVPEASEREG 17
Db 128 DVGPIPKIEKSEBEG 144

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RESULT 14
CREM_RAT
ID CREM_RAT STANDARD; PRT; 341 AA.
AC Q03061;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE CAMP responsive element modulator.
GN CREM.
OC Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

RESULT 15
R2_CORGL
ID R2_CORGL STANDARD; PRT; 368 AA.
AC OBN578;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Peptide chain release factor 2 (RF-2).

```

```

GN PRB OR CGL0801.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteriales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxId=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."
RL Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: Peptide chain release factor 2 directs the termination
CC of translation in response to the peptide chain termination codons
CC UGA and UAA (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE PROKARYOTIC AND MITOCHONDRIAL RELEASE
CC FACTORS FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AP005276; BAB38194.1; -.
DR HAMAP; MF_00094; -; 1.
DR InterPro; IPR005139; PCR_F.
DR InterPro; IPR000352; Pep_rel_factor_1.
DR InterPro; IPR004374; PRFB.
DR Pfam; PF03462; PCR_F; 1.
DR Pfam; PF00472; RF-1; 1.
DR TIGRFAMs; TIGR00020; prfb; 1.
DR PROSITE; PS00745; RF_PROX_1; 1.
*RM Protein biosynthesis; Complete proteome.
SQ SEQUENCE 368 AA; 41137 MW; C94D86D050AC5230 CRC64;

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Query Match 42.6%; Score 43; DB 1; Length 368;

Best Local Similarity 50.0%; Pred. No. 37;

Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

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OY 2 VEDVKKVEPASEREG 17
   :|:|:|:|:|:|:|
Db 75 IEDLPIMVELAEBDQ 90

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Search completed: August 1, 2003, 18:27:43
Job time : 14 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 1, 2003, 18:27:50 ; Search time 39 seconds
(without alignments)
49.317 Million cell updates/sec

Title: US-10-017-168-15

Perfect score: 101

Sequence: 1 EVEDVPKVEPASEGGER 20

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	97	96.0	256	2	F71326
2	82	81.2	227	2	G71326
3	51.5	51.0	153	1	B69215
4	50	49.5	184	2	D84603
5	48	47.5	547	2	E70650
6	47	46.5	308	2	T17946
7	47	46.5	1151	2	T24541
8	46.5	46.0	946	2	D66503
9	46	45.5	437	2	C51147
10	45	44.6	99	2	A55819
11	45	44.6	178	2	B95994
12	45	44.6	264	1	G69884
13	45	44.6	798	2	T33022
14	45	44.6	873	2	T16282
15	45	44.6	1350	2	G36793
16	44	43.6	220	1	S26685
17	44	43.6	251	1	C36044
18	44	43.6	306	2	T00177
19	44	43.6	306	2	G89888
20	44	43.6	344	2	JC5601
21	44	43.6	344	2	JC5602
22	44	43.6	681	2	B81815
23	44	43.6	682	1	E69200
24	44	43.6	897	2	E69202
25	44	43.6	1069	2	T00043
26	44	43.6	1072	2	T00041
27	44	43.6	1200	2	T00042
28	44	43.6	1537	2	JC4172
29	43	42.6	133	2	T36525

30	43	42.6	199	2	AB2847	conserved hypothet
31	43	42.6	210	2	CG7305	hypothetical prote
32	43	42.6	217	2	C37944	CAMP response elem
33	43	42.6	220	2	A75287	response regulator
34	43	42.6	227	2	B97624	hypothetical prote
35	43	42.6	229	2	B37944	CAMP response elem
36	43	42.6	229	2	A37944	CAMP response elem
37	43	42.6	278	2	S36101	CAMP response elem
38	43	42.6	341	2	S20827	CAMP response elem
39	43	42.6	341	2	S26886	CAMP response elem
40	43	42.6	356	2	B71023	hypothetical prote
41	43	42.6	369	2	A39157	probable RNA helic
42	43	42.6	434	2	T47545	monodehydroascorba
43	43	42.6	542	2	E84250	acetyl-CoA synthet
44	43	42.6	668	1	Q08EW1	US2 protein - hum
45	43	42.6	670	1	YCMU	acetoacetate synth

ALIGNMENTS

RESULT 1

F71326

hypothetical protein TP0433 - syphilis spirochete

C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999

C:Accession: F71326

R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin

rson, J.; Khalek, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; McDo

ney, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998

A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A:Reference number: A71250; MUID:98332770; PMID:9665876

A:Accession: F71326

A:Status: Preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-256 <COL>

A:Cross-references: GB:AE001220; GB:AE000520; NID:G3322705; PIDN:AC65421.1; PID:G332271

A:Experimental source: Brain Nichols

C:Genetic8:

A:Gene: TP0433

Query Match

Best Local Similarity 96.0%; Score 97; DB 2; Length 256;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy

1 EVEDVPKVEPASEGGER 20

Db

184 EVEDVPKVEPASEGGER 203

RESULT 2

G71326

hypothetical protein TP0434 - syphilis spirochete

C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999

C:Accession: G71326

R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin

rson, J.; Khalek, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; McDo

ney, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998

A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A:Reference number: A71250; MUID:98332770; PMID:9665876

A:Accession: G71326

A:Status: Preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-227 <COL>

A:Cross-references: GB:AE001220; GB:AE000520; NID:G3322705; PIDN:AC65422.1; PID:G332271

A:Experimental source: Brain Nichols

C:Genetic8:

A:Gene: TP0434

Query Match

81.2%; Score 82; DB 2; Length 227;

C:Genetics:
A:Gene: CESP:T05F1.6a
A:Map position: 1
A:Introns: 9/1; 21/2; 43/3; 186/3; 483/2; 574/3; 611/1; 957/3; 1029/2; 1124/3

Query Match 46.5%; Score 47; DB 2; Length 1151;
Best Local Similarity 45.0%; Pred. No. 64;
Matches 9; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy 1 EVEDVPKVEPASEREGGER 20
Db 659 EMEADPATATPASPNSRKRK 678

RESULT 8

D96503
protein P9C16.9 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: D96503
R:Theologian, A.; Becker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luo, J.S.; Matli, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A66141; MUID:21016719; PMID:11130712
A:Accession: D96503
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-946 <STO>
A:Cross-references: GB:AEO05173; NID:98778679; PIDN:AAF9687.1; GSPDB:GN00141
C:Genetics:
A:Gene: P9C16.9
A:Map position: 1

Query Match 46.0%; Score 46.5; DB 2; Length 946;
Best Local Similarity 47.8%; Pred. No. 63;
Matches 11; Conservative 4; Mismatches 5; Indels 3; Gaps 1;

Qy 1 EVEDVPK--VEPASEREGGER 20
Db 24 EADVPQVLDVDPKSNKSRK 46

RESULT 9

C35147
integrase homolog - Saccharopolyspora erythraea
C:Species: Saccharopolyspora erythraea
C>Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 22-Oct-1999
C:Accession: C35147
R:Brown, D.P.; Idler, K.B.; Katz, L.
J. Bacteriol. 172, 1877-1888, 1990
A>Title: Characterization of the genetic elements required for site-specific integration
A:Reference number: A35147; MUID:90202705; PMID:2180909
A:Accession: C35147
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-437 <BRO>
A:Cross-references: GB:M35138; NID:9152671; PIDN:AA98345.1; PID:9152674

Query Match 45.5%; Score 46; DB 2; Length 437;
Best Local Similarity 50.0%; Pred. No. 33;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 EVEDVPKVEPASEREGGER 20
Db 185 EVEDQVLVIKALERRNGVR 204

RESULT 10
A55819
nonhistone chromosomal protein CHMG-I - midge (Chironomus tentans)

N:Alternate names: high mobility group protein I/Y homolog
C:Species: Chironomus tentans
C>Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 21-Jul-2000
C:Accession: A55819; S47253; S47252
R:Claus, P.; Schulze, E.; Wisniewski, J.R.
J. Biol. Chem. 269, 33042-33048, 1994

A>Title: Insect proteins homologous to mammalian high mobility group proteins I/Y (HMG I
A:Reference number: A55819; MUID:95105193; PMID:7806532
A:Accession: A55819
A:Molecule type: mRNA

A:Cross-references: EMBL:Z36898; NID:9534932; PIDN:CAA65365.1; PID:9534933
A:Experimental source: clone pCM126
R:Claus, P.; Schulze, E.; Wisniewski, J.R.
submitted to the EMBL Data Library, August 1994
A:Description: Insect proteins homologous to mammalian high mobility group proteins I/Y
A:Reference number: S47252
A:Accession: S47253
A:Molecule type: DNA

A:Residues: 1-91, 'A', 93-99 <CL2>
A:Cross-references: EMBL:Z36897; NID:9534886; PID:9534887
A:Experimental source: clone pCWG106
C:Genetics:
A:Introns: 15/3; 76/1

A>Note: suggested by Southern blot analysis in Ref A55819 to be single copy gene
C:Keywords: chromosomal protein; DNA binding
F:8-13/Region: DNA-binding motif (K/R-G-R-G-R-P)
F:55-60/Region: DNA-binding motif (K/R-G-R-G-R-P)
F:75-80/Region: DNA-binding motif (K/R-G-R-G-R-P)

Query Match 44.6%; Score 45; DB 2; Length 99;
Best Local Similarity 44.4%; Pred. No. 10;
Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EVEDVPKVEPASEREGG 18
Db 33 KVEEVPKIEESTPEENG 50

RESULT 11

E95994
hypotheetical protein [imported] - Sinorhizobium meliloti (strain 1021) magaplaemid pSymB
C:Species: Sinorhizobium meliloti
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C:Accession: E95994
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Herman
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A>Title: The complete sequence of the 1,663-kb pSymB magaplaemid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11461431
A:Accession: E95994
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-178 <KIR>
A:Cross-references: GB:A5591985; PIDN:CAQ49621.1; PID:915141108; GSPDB:GN00167
A:Experimental source: strain 1021, magaplaemid pSymB
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federpiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaulic, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yen, K.

A>Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: Smb21395
A:Genome: plasmid

Query Match 44.6%; Score 45; DB 2; Length 178;
Best Local Similarity 44.4%; Pred. No. 10;
Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Best Local Similarity 41.2%; Pred. No. 19;
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 2 VEDVPKVEPASEREGG 18
Db 157 IEPITLAEPEDEPGG 173

RESULT 12

conserved hypothetical protein ymdB - Bacillus subtilis
G69884

C:Species: Bacillus subtilis
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000

C:Accession: G69884
R:Kumet, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerison, P.T.; Estlin, K.D.; Evington, J.; Fabret, C.; Ferrari, E.
Nature 350, 249-256, 1997

A:Authors: Foulger, D.; Fultz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
leoh, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koester, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y.M.; Ogawa, K.; Ogawa, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Kieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,
A:Authors: Schlicht, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
Akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zmesstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; PMID:9804033; PMID:9384377

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Accession: G69884

A:Residues: 1-264 <KUN>
A:Molecule type: DNA

A:Cross-references: GB:299112; GB:AL009126; NID:g2633902; PIDN:CAB13570.1; PID:g2634069
A:Experimental source: strain 168

C:Genetics:
A:Gene: ymdB

C:Superfamily: hypothetical protein ymdB

Query Match 44.6%; Score 45; DB 1; Length 264;
Best Local Similarity 50.0%; Pred. No. 28;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 VEDVPKVEPASEREGG 17
Db 79 IDVPVLVPPANPEG 94

RESULT 13

T33022
hypothetical protein K07H8.10 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C:Accession: T33022
R:Fulton, B.; Hawkins, J.; Gattung, S.; Wohldmann, P.; Elliott, G.
submitted to the EMBL Data Library, February 1998

A:Description: The sequence of C. elegans cosmid K07H8.
A:Reference number: Z21264

A:Accession: T33022
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-798 <FUL>

A:Cross-references: EMBL:AF047659; PIDN:AG04430.1; GSPDB:GN00022; CESP:K07H8.10
C:Genetics:
A:Gene: CESP:K07H8.10

A:Map position: 4
A:introns: 205/1; 308/3; 630/1; 773/3

Query Match 44.6%; Score 45; DB 2; Length 798;
Best Local Similarity 44.4%; Pred. No. 89;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EVEDVPKVEPASEREGG 18
Db 500 EEDIPAVKPKTERKGG 517

RESULT 14

T16282
hypothetical protein F35H10.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 24-Nov-1999

C:Accession: T16282
R:Moessner, J.
submitted to the EMBL Data Library, November 1995

A:Description: The sequence of C. elegans cosmid F35H10.
A:Reference number: 218490

A:Accession: T16282
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-873 <MOE>

A:Cross-references: EMBL:U40934; NID:g1072149; PID:g1072154; PIDN:AAA81682.1; CESP:F35H10.4
A:Gene: CESP:F35H10.4

A:introns: 39/3; 709/3; 785/1; 843/2
C:Superfamily: vacuolar ATP synthase 95K chain

Query Match 44.6%; Score 45; DB 2; Length 873;
Best Local Similarity 56.2%; Pred. No. 98;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 VEDVPKVEPASEREGG 17
Db 333 VEDVPKVEPASEREGG 348

RESULT 15

G36793
hypothetical protein ORF72 - ictalurid herpesvirus 1 (strain auburn 1)

C:Species: ictalurid herpesvirus 1
A:Note: host ictalurid punctatus (channel catfish)

C:Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 24-Nov-1999
C:Accession: G36793

R:Davidson, A.J.
submitted to GenBank, January 1992

A:Description: Channel catfish virus: a new type of herpesvirus.
A:Reference number: A36804

A:Accession: G36793
A:Molecule type: DNA

A:Residues: 1-1350 <DAV>
A:Cross-references: GB:M75136; NID:g331209; PIDN:AAA8174.1; PID:g331280

R:Davidson, A.J.
Virology 186, 9-14, 1992

A:Title: Channel catfish virus: a new type of herpesvirus.
A:Reference number: A39447; PMID:92087490; PMID:1727613

A:Contents: annotation
A:Note: neither protein nor nucleic acid sequence is given

C:Genetics:
A:Gene: 72

C:Superfamily: ictalurid herpesvirus 1 hypothetical protein ORF72

Query Match 44.6%; Score 45; DB 2; Length 1350;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 3 EDVPKVEPASEREGG 20
Db 913 KSVKRIEASMEGGER 930

Search completed: August 1, 2003, 18:38:00
Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: August 1, 2003, 18:37:21 ; Search time 21 seconds
(without alignments)
113.105 Million cell updates/sec

Title: US-10-017-168-15
Perfect score: 101
Sequence: 1 EVEDPKVPEASREGER 20

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PTCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	48.5	266	US-10-036-542-66	Sequence 66, App1
2	49	48.5	277	US-10-036-542-92	Sequence 92, App1
3	49	48.5	277	US-10-036-542-134	Sequence 134, App1
4	49	48.5	288	US-10-036-542-130	Sequence 130, App1
5	49	48.5	304	US-09-925-300-1615	Sequence 1615, App1
6	44	43.6	71	US-09-864-761-35920	Sequence 35920, App1
7	44	43.6	268	US-09-764-864-1172	Sequence 1172, App1
8	44	43.6	392	US-10-156-761-10989	Sequence 10989, App1
9	44	43.6	1038	US-09-752-639-151	Sequence 151, App1
10	44	43.6	1038	US-09-984-198-151	Sequence 151, App1
11	43	42.6	57	US-10-211-088-109	Sequence 109, App1
12	43	42.6	178	US-09-764-864-1091	Sequence 1091, App1
13	43	42.6	241	US-09-738-626-5590	Sequence 5590, App1
14	43	42.6	266	US-10-102-806-605	Sequence 605, App1
15	43	42.6	368	US-09-738-626-4393	Sequence 4393, App1

16	43	42.6	670	US-10-057-609B-3	Sequence 3, App1
17	43	42.6	670	US-10-004-827-3	Sequence 4, App1
18	43	42.6	670	US-10-004-827-4	Sequence 4, App1
19	43	42.6	670	US-10-004-827-26	Sequence 26, App1
20	43	42.6	811	US-09-840-787-45	Sequence 45, App1
21	42	41.6	295	US-09-975-719-341	Sequence 341, App1
22	41.5	41.1	554	US-09-815-242-5728	Sequence 5728, App1
23	41.5	41.1	1592	US-09-815-242-12160	Sequence 12160, App1
24	41.5	41.1	1592	US-09-832-292-35	Sequence 35, App1
25	41	40.6	249	US-09-815-242-11658	Sequence 11658, App1
26	41	40.6	285	US-10-156-761-13708	Sequence 13708, App1
27	41	40.6	554	US-09-746-491-41	Sequence 41, App1
28	41	40.6	749	US-10-211-962-98	Sequence 98, App1
29	41	40.6	1106	US-10-157-931-30	Sequence 30, App1
30	41	40.6	5215	US-09-861-289-2	Sequence 2, App1
31	41	40.6	5215	US-09-860-846-2	Sequence 2, App1
32	41	40.6	5215	US-09-888-384B-2	Sequence 2, App1
33	41	40.6	5215	US-09-836-821-2	Sequence 2, App1
34	40.5	40.1	59	US-09-967-237-50	Sequence 50, App1
35	40.5	40.1	98	US-09-772-719-50	Sequence 50, App1
36	40.5	40.1	377	US-09-967-237-87	Sequence 87, App1
37	40.5	40.1	459	US-09-772-719-2	Sequence 2, App1
38	40.5	40.1	459	US-09-967-237-2	Sequence 2, App1
39	40.5	40.1	610	US-09-783-708-1	Sequence 1, App1
40	40	39.6	26	US-09-864-761-38892	Sequence 38892, App1
41	40	39.6	114	US-09-796-692-2447	Sequence 2447, App1
42	40	39.6	114	US-10-040-862-2447	Sequence 2447, App1
43	40	39.6	315	US-10-245-103-44	Sequence 44, App1
44	40	39.6	315	US-10-245-107-44	Sequence 44, App1
45	40	39.6	315	US-10-245-143-44	Sequence 44, App1

ALIGNMENTS

RESULT 1
US-10-036-542-66
; Sequence 66, Application US/10036542
; Publication No. US20030083481A1
; GENERAL INFORMATION:
; APPLICANT: Bire et al.
; TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
; FILE REFERENCE: PA00201
; CURRENT APPLICATION NUMBER: US/10/036,542
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: PCT/US00/19666
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/144,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 60/148,681
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/149,173
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/158,004
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 60/194,689
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 66
; LENGTH: 266
; TYPE: PRT
; ORGNISM: Homo sapiens
US-10-036-542-66
Query Match 48.5%; Score 49; DB 15; Length 266;
Best Local Similarity 53.3%; Pred. No. 12;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 4 DVKPKVPEASREGER 18
DB 238 EIPKVFDEKERESG 252

```
RESULT 2
US-10-036-542-92
; Sequence 92, Application US/10036542
; Publication No. US20030083481A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
; FILE REFERENCE: PA002P1
; CURRENT APPLICATION NUMBER: US/10/036,542
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: PCT/US00/19666
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/144,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 60/148,681
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/149,173
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/158,004
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 60/194,689
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 92
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (147)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-036-542-92

Query Match      48.5%; Score 49; DB 15; Length 277;
Best Local Similarity 53.3%; Pred. No. 13;
Matches      8; Conservative      3; Mismatches      4; Indels      0; Gaps      0;

QY      4 DVPKVEPASEREGG 18
Db      238 EIKPVDPKEREBSG 252

RESULT 3
US-10-036-542-134
; Sequence 134, Application US/10036542
; Publication No. US20030083481A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
; FILE REFERENCE: PA002P1
; CURRENT APPLICATION NUMBER: US/10/036,542
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: PCT/US00/19666
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/144,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 60/148,681
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/149,173
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/158,004
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 60/194,689
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 134
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: SITE
; LOCATION: (147)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-036-542-134

Query Match      48.5%; Score 49; DB 15; Length 277;
Best Local Similarity 53.3%; Pred. No. 13;
Matches      8; Conservative      3; Mismatches      4; Indels      0; Gaps      0;

QY      4 DVPKVEPASEREGG 18
Db      238 EIKPVDPKEREBSG 252

RESULT 4
US-10-036-542-130
; Sequence 130, Application US/10036542
; Publication No. US20030083481A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
; FILE REFERENCE: PA002P1
; CURRENT APPLICATION NUMBER: US/10/036,542
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: PCT/US00/19666
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/144,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 60/148,681
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/149,173
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/158,004
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 60/194,689
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 130
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-036-542-130

Query Match      48.5%; Score 49; DB 15; Length 288;
Best Local Similarity 53.3%; Pred. No. 13;
Matches      8; Conservative      3; Mismatches      4; Indels      0; Gaps      0;

QY      4 DVPKVEPASEREGG 18
Db      261 EIKPVDPKEREBSG 275

RESULT 5
US-09-925-300-1615
; Sequence 1615, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1615
; LENGTH: 304
; TYPE: PRT
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (174)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1615

Query Match
Best Local Similarity 48.5%; Score 49; DB 10; Length 304;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 EDVKVPEPASEREGG 18
Db 265 EIPKVFDEKERESG 279

RESULT 6
US-09-864-761-35920
; Sequence 35920, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmics-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 35920
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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; OTHER INFORMATION: MAP TO AC006146.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.4
; OTHER INFORMATION: EST_HUMAN HIT: A1702990.1, EVALU8 7.20e-02
US-09-864-761-35920

Query Match
Best Local Similarity 43.6%; Score 44; DB 9; Length 71;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 3 EDVKVPEPASEREGG 20
Db 36 EVPEIQEKQEBGRER 53

RESULT 7
US-09-764-864-1172
; Sequence 1172, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; PRIOR application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1172
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (58)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (261)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (1262)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1172

Query Match
Best Local Similarity 43.6%; Score 44; DB 10; Length 268;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 3 EDVKVPEPASEREGG 20
Db 185 EVPEIQEKQEBGRER 202

RESULT 8
US-10-156-761-10989
; Sequence 10989, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
```

FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 10989
LENGTH: 392
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-10989

Query Match
Best Local Similarity 43.6%; Score 44; DB 15; Length 392;
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 EVEDVPKVEPASEEGE 19
DB 23 EVIDTPEARAEATERLGGK 41

RESULT 9
US-09-752-639-151
Sequence 151, Application US/09752639
Patent No. US20020091243A1
GENERAL INFORMATION:
APPLICANT: Gatanaga, T.
APPLICANT: Granger, G.A.
TITLE OF INVENTION: Factors Altering Tumor Necrosis
TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: PasteSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/752,639
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/10793
FILING DATE:
APPLICATION NUMBER: 09/081,385
FILING DATE:
APPLICATION NUMBER: 08/964,747
FILING DATE: 05-NOV-1997
APPLICATION NUMBER: 60/030,761
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Wu, Frank
REGISTRATION NUMBER: 41,386
REFERENCE/DOCKET NUMBER: 22000-20577.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 151:
SEQUENCE CHARACTERISTICS:
LENGTH: 1038 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
US-09-752-639-151

Query Match
Best Local Similarity 43.6%; Score 44; DB 9; Length 1038;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 3 EDVPKVEPASEEGE 20
DB 954 EEVPEIQEKEQEGGR 971

RESULT 10
US-09-984-198-151
Sequence 151, Application US/09984198
Patent No. US20020106679A1
GENERAL INFORMATION:
APPLICANT: Gatanaga, T.
APPLICANT: Granger, G.A.
TITLE OF INVENTION: Factors Altering Tumor Necrosis
TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: PasteSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,198
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/10793
FILING DATE:
APPLICATION NUMBER: 09/081,385
FILING DATE:
APPLICATION NUMBER: 08/964,747
FILING DATE: 05-NOV-1997
APPLICATION NUMBER: 60/030,761
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Wu, Frank
REGISTRATION NUMBER: 41,386
REFERENCE/DOCKET NUMBER: 22000-20577.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 151:
SEQUENCE CHARACTERISTICS:
LENGTH: 1038 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-984-198-151

Query Match
Best Local Similarity 43.6%; Score 44; DB 10; Length 1038;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 3 EDVPKVEPASEEGE 20
DB 954 EEVPEIQEKEQEGGR 971

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RESULT 11
US-10-211-088-109
; Sequence 109, Application US/102211088
; Publication No. US20030104479A1
; GENERAL INFORMATION:
; APPLICANT: Bright, Gary R.
; APPLICANT: Premkumar, D. David
; TITLE OF INVENTION: No. US20030104479A1 Fusion Proteins And Assays For Molecular B
; FILE REFERENCE: 01-1022-US
; CURRENT APPLICATION NUMBER: US/10/211,088
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/309,395
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/341,589
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: Patentin ver. 3.1
; SEQ ID NO 109
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Binding domain
US-10-211-088-109

Query Match          42.6%; Score 43; DB 15; Length 57;
Best Local Similarity 47.1%; Pred. No. 17;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 EVDVYKVPASEREG 17
   |||:|:|:|:|:|
Db 39 DVPGIPKIEEKSEEG 55

RESULT 12
US-09-764-864-1091
; Sequence 1091, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT23
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1091
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-1091

Query Match          42.6%; Score 43; DB 10; Length 178;
Best Local Similarity 53.3%; Pred. No. 62;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 6 PKVPEASEREGGER 20
   ||:|:|:|:|
Db 129 PRLSVPAAREGAR 143

RESULT 13
US-09-738-626-6590
; Sequence 6590, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIO
; APPLICANT: OCHIAI, KEIKO
```

```
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: Patentin ver. 3.0
; SEQ ID NO 6590
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6590

Query Match          42.6%; Score 43; DB 10; Length 241;
Best Local Similarity 56.2%; Pred. No. 87;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 DVPKVPASEREGGE 19
   |||:|:|:|:|
Db 78 DVPKVPASEREGGE 93

RESULT 14
US-10-102-806-605
; Sequence 605, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103P1C1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 605
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (84)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-102-806-605

Query Match          42.6%; Score 43; DB 15; Length 266;
Best Local Similarity 56.2%; Pred. No. 97;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 EDVPEVPEASEREGG 18
   ||:|:|:|:|
Db 140 EDNPEVVRPHNGRVGG 155

RESULT 15
US-09-738-626-4393
; Sequence 4393, Application US/09738626
; Publication No. US20020197605A1
```

/ GENERAL INFORMATION:
/ APPLICANT: NAKAGAWA, SATOSHI
/ APPLICANT: MIZOGUCHI, HIROSHI
/ APPLICANT: ANDO, SEIKO
/ APPLICANT: HAYASHI, MIKIRO
/ APPLICANT: OCHIAI, KEIKO
/ APPLICANT: YOKOI, HARUHIKO
/ APPLICANT: TATEISHI, NAKO
/ APPLICANT: SENOH, AKIHIRO
/ APPLICANT: IKEDA, MASATO
/ APPLICANT: OZAKI, AKIO
/ TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
/ FILE REFERENCE: 249-125
/ CURRENT APPLICATION NUMBER: US/09/738,626
/ CURRENT FILING DATE: 2000-12-18
/ PRIOR APPLICATION NUMBER: JP 99/377484
/ PRIOR FILING DATE: 1999-12-16
/ PRIOR APPLICATION NUMBER: JP 00/159162
/ PRIOR FILING DATE: 2000-04-07
/ PRIOR APPLICATION NUMBER: JP 00/280988
/ PRIOR FILING DATE: 2000-08-03
/ NUMBER OF SEQ ID NOS: 7059
/ SOFTWARE: PatentIn ver. 3.0
/ SEQ ID NO 4393
/ LENGTH: 368
/ TYPE: PRT
/ ORGANISM: Corynebacterium glutamicum
US-09-738-626-4393

Query Match 42.6%; Score 43; DB 10; Length 368;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
Qy 2 VEDVPKVVEPASREG 17
Db 75 IEDLPTWELAEEDG 90

Search completed: August 1, 2003, 18:45:48
Job time : 23 secs

US-09-163-748C-7

Query Match 46.5%; Score 47; DB 4; Length 117;
Best Local Similarity 46.7%; Pred. No. 2.8;
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 3 EDVVKVEPASEREG 17
:|||||:|
DB 30 DEVEMIEPATREG 44

RESULT 3

US-09-252-991A-26148
; Sequence 26148, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26148
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26148

Query Match 46.0%; Score 46.5; DB 4; Length 571;
Best Local Similarity 64.7%; Pred. No. 21;
Matches 11; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 5 VP-KVEPASEREG 20
:|||||:|
DB 74 VPQVVEPAAARQGER 90

RESULT 4

US-09-252-991A-32898
; Sequence 32898, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32898
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32898

Query Match 43.6%; Score 44; DB 4; Length 228;
Best Local Similarity 62.5%; Pred. No. 18;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 VEDVVKVEPASEREG 17
:|||||:|
DB 74 VEHVGVVEPLSRGHG 89

RESULT 5

US-09-035-648-18
; Sequence 18, Application US/09035648
; Patent No. 6100031
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: DIAGNOSIS, PREVENTION, AND TREATMENT OF NEOPLASTIC CELL
; TITLE OF INVENTION: GROWTH AND PROLIFERATION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/035,648

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/818,829

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Melkielejohn, Ph.D., Anita L.

REGISTRATION NUMBER: 35,283

REFERENCE/DOCKET NUMBER: 07334/003001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070

TELEFAX: 617-542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 747 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

US-09-035-648-18

Query Match 43.6%; Score 44; DB 3; Length 747;
Best Local Similarity 50.0%; Pred. No. 72;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 VEDVVKVEPASEREG 19
:|||||:|
DB 51 VGDVFPQKPASTDTEGDD 68

RESULT 6

US-09-001-951-18
; Sequence 18, Application US/09001951
; Patent No. 6268470
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: DIAGNOSIS, PREVENTION, AND TREATMENT OF NEOPLASTIC CELL
; TITLE OF INVENTION: GROWTH AND PROLIFERATION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/001,951
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/818,829
FILING DATE: 14-MAR-1997
APPLICATION NUMBER: 60/013,438
FILING DATE: 15-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Melkielejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 747 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-001-951-18

Query Match 43.6%; Score 44; DB 3; Length 747;
Best Local Similarity 50.0%; Pred. No. 72;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 VEDVPKVEPASPAREGCE 19
DB 51 VGDVPFOLKPASDTEGDQ 68

RESULT 7
US-08-818-829-18
Sequence 18, Application US/08818829
Patent No. 6458939
GENERAL INFORMATION:
APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS, PREVENTION, AND TREATMENT OF NEOPLASTIC CELL
NUMBER OF INVENTION: GROWTH AND PROLIFERATION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,829
FILING DATE: 14-MAR-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/013,438
FILING DATE: 15-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Melkielejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/003001
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 747 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-818-829-18

Query Match 43.6%; Score 44; DB 4; Length 747;
Best Local Similarity 50.0%; Pred. No. 72;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 VEDVPKVEPASPAREGCE 19
DB 51 VGDVPFOLKPASDTEGDQ 68

RESULT 8
US-08-363-208-2
Sequence 2, Application US/08363208
Patent No. 5767366
GENERAL INFORMATION:
APPLICANT: Sathasivan, Kanagasabapathi
TITLE OF INVENTION: A Mutant Acetolactate Synthase Gene From
TITLE OF INVENTION: Arabidopsis Thaliana For Confering Imdazolione
NUMBER OF INVENTION: Resistance To Crop Plants
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Llewellyn A. Proctor, Sr.
STREET: 11481 Sheraton Drive
CITY: Baton Rouge,
STATE: LA
COUNTRY: USA
ZIP: 70815
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,208
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,429
FILING DATE: 19-FEB-1991
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Proctor Sr., Llewellyn A.
REGISTRATION NUMBER: 20,152
REFERENCE/DOCKET NUMBER: 013911-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (504)275-8689
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 670 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-363-208-2

Query Match 42.6%; Score 43; DB 1; Length 670;
Best Local Similarity 50.0%; Pred. No. 91;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVEDVPKVEPAPA 12
DB 227 DVEDIPRIIEEA 238

RESULT 9
US-09-137-478-2
Sequence 2, Application US/09137478
Patent No. 6225105
GENERAL INFORMATION:
APPLICANT: Sachaivan, Kanagasabapathi
APPLICANT: Murali, No. 6225105imoto
TITLE OF INVENTION: A Mutant Acetolactate Synthase Gene From
TITLE OF INVENTION: Arabidopsis thaliana For Conferring Imidazolinone
TITLE OF INVENTION: Resistance To Crop Plants
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Llewellyn A. Proctor, Sr.
STREET: 11481 Sheraton Drive
CITY: Baton Rouge,
STATE: LA
COUNTRY: USA
ZIP: 70815
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/137,478
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,429
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Proctor Sr., Llewellyn A.
REGISTRATION NUMBER: 20,152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (504)275-8689
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 670 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-137-478-2

Query Match 42.6%; Score 43; DB 3; Length 670;
Best Local Similarity 50.0%; Pred. No. 91;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVEDVPKVVPEA 12
:||||:|
Db 227 DVEDIPRIIEA 238

RESULT 10
US-08-426-125-8
Sequence 8, Application US/08426125
Patent No. 5853973
GENERAL INFORMATION:
APPLICANT: Kakefuda, Genichi
APPLICANT: Otc, Karl-Heinz
APPLICANT: Kwagh, Jae-Gyu
APPLICANT: Stockton, Gerald W.
TITLE OF INVENTION: Structure-Based Designed Herbicide
TITLE OF INVENTION: Resistant Products
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA

ZIP: 10022-7513
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,125
FILING DATE: 20-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robinson, Joseph
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 0646/0A674
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)-527-7783
TELEFAX: (212)-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 671 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Arabidopsis thaliana
US-08-426-125-8

Query Match 42.6%; Score 43; DB 2; Length 671;
Best Local Similarity 50.0%; Pred. No. 92;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVEDVPKVVPEA 12
:||||:|
Db 227 DVEDIPRIIEA 238

RESULT 11
US-08-455-355-8
Sequence 8, Application US/08455355
Patent No. 5928937
GENERAL INFORMATION:
APPLICANT: Kakefuda, Genichi
APPLICANT: Otc, Karl-Heinz
APPLICANT: Kwagh, Jae-Gyu
APPLICANT: Stockton, Gerald W.
TITLE OF INVENTION: Structure-Based Designed Herbicide
TITLE OF INVENTION: Resistant Products
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022-7513
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,355
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robinson, Joseph
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 0646/1A674-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)-527-7783

```

;
; TELEFAX: (212)-753-6237
;
; TELETYPE: 236687
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 671 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Arabidopsis thaliana
; US-08-455-355-8

Query Match          42.6%; Score 43; DB 2; Length 671;
Best Local Similarity 50.0%; Pred. No. 92;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      1 EYEDVPKVVEPA 12
Db      227 DVEDIPRIIEEA 238

RESULT 12
US-09-367-512-7
; Sequence 7, Application US/09367512
; Patent No.: 6576455
; GENERAL INFORMATION:
; APPLICANT: American Cyanamid Company
; APPLICANT: Kakefuda, Genichi
; APPLICANT: Otc, Karl-Heinz
; APPLICANT: Kwagh, Jae-Gyu.
; APPLICANT: Stockton, Gerald W.
; TITLE OF INVENTION: Structure-Based Designed Herbicide Resistant
; FILE REFERENCE: 3489/1A674-US3
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 08/426,125
; PRIOR FILING DATE: 1995-04-20
; PRIOR APPLICATION NUMBER: 08/455,355
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: PCT/US96/05782
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 671
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-09-367-512-7

Query Match          42.6%; Score 43; DB 4; Length 671;
Best Local Similarity 50.0%; Pred. No. 92;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      1 EYEDVPKVVEPA 12
Db      227 DVEDIPRIIEEA 238

RESULT 13
US-09-046-894-35
; Sequence 35, Application US/09046894
; Patent No.: 6190857
; GENERAL INFORMATION:
; APPLICANT: Ralph, David
; APPLICANT: An, Gang
; APPLICANT: O'Hara, Mark S.
; APPLICANT: Veltri, Robert
; TITLE OF INVENTION: DIAGNOSIS OF DISEASE STATE USING mRNA
; TITLE OF INVENTION: PROFILES IN PERIPHERAL LEUKOCYTES
; NUMBER OF SEQUENCES: 55

```

```

;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,894
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/041,576
; FILING DATE: 24-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakashima, Richard A.
; REGISTRATION NUMBER: P-42,023
; REFERENCE/DOCKET NUMBER: UROC:014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 761 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-046-894-35

Query Match          42.6%; Score 43; DB 3; Length 761;
Best Local Similarity 41.2%; Pred. No. 1.1e+02;
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      4 DVPKVEPASERREGGR 20
Db      727 DTPATDPLSEKGGKK 743

```

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RESULT 14
US-08-933-750C-45
; Sequence 45, Application US/08933750C
; Patent No.: 5932442
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Bandman, Olga
; APPLICANT: Shah, Purvi
; APPLICANT: Au-Young, Janice
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,750C
; FILING DATE: September 23, 1997

```

```
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0356 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 45:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 811 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: L1VRUT04
/ CLONE: 2515476
/
/ US-08-933-750C-45
/
Query Match 42.6%; Score 43; DB 2; Length 811;
Best Local Similarity 41.2%; Pred. No. 1.1e+02;
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 4 DVPKVEPASEREGGER 20
DB 777 DTPATSDPLSEKGGKK 793

RESULT 15
/ US-09-234-613-45
/ Sequence 45, Application US/09234613
/ Patent No. 6132973
/ GENERAL INFORMATION:
/ APPLICANT: Lal, Preeti
/ APPLICANT: Hillman, Jennifer L.
/ APPLICANT: Bandman, Olga
/ APPLICANT: Shah, Purni
/ APPLICANT: Au-Young, Janice
/ APPLICANT: Yue, Henry
/ APPLICANT: Guegler, Karl J.
/ APPLICANT: Corley, Neil C.
/ TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
/ NUMBER OF SEQUENCES: 98
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FASTSEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/234,613
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/933,750
/ FILING DATE: September 23, 1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0356 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
```

```
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 45:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 811 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: L1VRUT04
/ CLONE: 2515476
/
/ US-09-234-613-45
/
Query Match 42.6%; Score 43; DB 3; Length 811;
Best Local Similarity 41.2%; Pred. No. 1.1e+02;
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 4 DVPKVEPASEREGGER 20
DB 777 DTPATSDPLSEKGGKK 793
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Search completed: August 1, 2003, 18:38:35
JOB time : 30 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 1, 2003, 18:22:55 ; Search time 41 Seconds
(without alignments)
77.428 Million cell updates/sec

Title: US-10-017-168-15

Perfect score: 101
Sequence: 1 EVEDVPKVEPASEREGGER 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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24:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	101	100.0	20	22	AAB48327	T. pallidum acidica
2	101	100.0	232	22	AAB48317	T. pallidum ssp. p
3	101	100.0	312	22	AAB48318	T. pallidum ssp. en
4	101	100.0	432	22	AAB48316	T. pallidum ssp. p
5	97	96.0	20	22	AAB48329	T. pallidum acidica
6	96	95.0	20	22	AAB48328	T. pallidum acidica
7	87	86.1	20	22	AAB48320	T. pallidum acidica
8	82	81.2	20	22	AAB48330	T. pallidum acidica
9	77	76.2	20	22	AAB48321	T. pallidum acidica

10	65	64.4	21	22	AAB48335	T. pallidum acid
11	60	59.4	19	22	AAB48335	T. pallidum acid
12	53	52.5	25	22	AAB48336	T. pallidum acid
13	50	49.5	79	21	AAG61681	Arabisopsis thalia
14	50	49.5	187	21	AAG16639	Arabisopsis thalia
15	50	49.5	187	21	AAG50350	Arabisopsis thalia
16	49	48.5	266	22	AAM93738	Human polyepicid
17	49	48.5	266	22	AAB80279	Human prostate can
18	49	48.5	266	22	AAB64379	Human acid sequenc
19	49	48.5	277	22	AAB80305	Human prostate can
20	49	48.5	277	22	AAB80347	Human prostate can
21	49	48.5	288	22	AAB80343	Human prostate can
22	49	48.5	289	22	AAM15524	Human polyepicid
23	49	48.5	304	21	AAB57037	Human prostate can
24	48	47.5	296	22	AAB51624	Novel human diagno
25	47.5	47.0	792	22	AAG62199	S. epidermidis ope
26	47.5	47.0	801	23	ABP40739	Staphylococcus epi
27	47	46.5	1022	22	ABG02687	Novel human diagno
28	47	46.5	1278	24	ABG74682	Human CGSD protei
29	46	45.5	60	23	ABP34774	Human ORF3747 prot
30	46	45.5	171	21	AAG08178	Arabisopsis thalia
31	46	45.5	197	21	AAG08177	Arabisopsis thalia
32	46	45.5	226	21	AAG08176	Arabisopsis thalia
33	45	44.6	197	21	AAG59487	Arabisopsis thalia
34	45	44.6	226	21	AAG59486	Arabisopsis thalia
35	45	44.6	286	21	AAG59485	Arabisopsis thalia
36	44	43.6	57	22	AAT47776	Propionibacterium
37	44	43.6	71	22	ABG50059	Human liver peptid
38	44	43.6	71	22	ABB350014	Peptide #2665 enco
39	44	43.6	71	22	ABB35183	Peptide #2689 enco
40	44	43.6	71	22	ABB20622	Protein #2621 enco
41	44	43.6	71	22	AAM65018	Human brain expres
42	44	43.6	71	22	AAM68385	Human bone marrow
43	44	43.6	71	22	AAM16202	Peptide #2636 enco
44	44	43.6	71	22	AAM28635	Peptide #2730 enco
45	44	43.6	71	22	AAM03955	Peptide #2617 enco

ALIGNMENTS

	RESULT 1
AA848327	
ID	AA848327 strand; peptide; 20 AA.
XX	
AC	AA848327;
XX	
DT	20-APR-2001 (first entry)
DE	T. pallidum acidic repeat protein immunogenic peptide arp 9.
XX	
KW	Treponema pallidum, acidic repeat protein; arp; immunogenic; syphilis yaws; bejel.
OS	Treponema pallidum.
XX	
PN	WO20077486-A2.
PD	
XX	21-DEC-2000.
PF	14-JUN-2000; 2000MO-US16425.
PR	14-JUN-1999; 99US-0138981.
XX	(USSH) US DEPT HEALTH & HUMAN SERVICES.
PI	Liu H, Steiner B, Rhodes B,
DR	WPI; 2001-080711/09.
XX	
FT	Detecting Treponema pallidum in blood, saliva, etc., by detecting formation of a complex between immunogenic peptides of acidic repeat protein of the bacterium and an antibody present in the biological

PT sample -
XX Claim 15; Fig 11; 73pp; English.
PS
XX
CC The invention relates to a method of detecting presence of Treponema
CC pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological
CC sample that involves contacting an acidic repeat protein (arp), or one
CC or more isolated immunogenic TP peptides of arp with an Ab containing
CC biological sample and then detecting the formation of a complex between
CC immunogenic peptides and Ab. The presence of the complex indicates the
CC presence of TP. The method is thus useful for diagnosing syphilis, yaws,
CC and bejel diseases. The immunogenic peptides or the Abs raised against
CC arp, as part of an immunogenic composition, are useful for inducing a
CC protective immune response against syphilis, yaws or bejel caused by TP.
CC Sequences AAB48319-AAB48330 represent immunogenic peptides of T. pallidum
CC arp protein.
XX
SQ Sequence 20 AA;
XX
Query Match 100.0%; Score 101; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 EVEDVPKVVPEPASEREGGER 20
DB 1 EVEDVPKVVPEPASEREGGER 20
XX
RESULT 2
AAB48317
ID AAB48317 standard; Protein; 232 AA.
XX
AC AAB48317;
XX
DT 20-APR-2001 (first entry)
XX
DE T. pallidum ssp. pertenue (CDC-2) acidic repeat protein (arp).
XX
KW Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;
KW yaws; bejel.
XX
OS Treponema pallidum ssp. pertenue.
XX
PN WO200077486-A2.
XX
PD 21-DEC-2000.
XX
XX 14-JUN-2000; 2000MO-US16425.
PF
XX 14-JUN-1999; 99US-0138981.
PR
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX Liu H, Steiner B, Rhodes B;
PI
XX WPI; 2001-080711/09.
DR
XX N-PSDB; AAC84648.
XX
PT Detecting Treponema pallidum in blood, saliva, etc., by detecting
PT formation of a complex between immunogenic peptides of acidic repeat
PT protein of the bacterium and an antibody present in the biological
PT sample -
XX
XX Claim 15; Fig 8; 73pp; English.
XX
CC The invention relates to a method of detecting presence of Treponema
CC pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological
CC sample that involves contacting an acidic repeat protein (arp), or one
CC or more isolated immunogenic TP peptides of arp with an Ab containing
CC biological sample and then detecting the formation of a complex between
CC immunogenic peptides and Ab. The presence of the complex indicates the
CC presence of TP. The method is thus useful for diagnosing syphilis, yaws,
CC and bejel diseases. The immunogenic peptides or the Abs raised against

CC arp, as part of an immunogenic composition, are useful for inducing a
CC protective immune response against syphilis, yaws or bejel caused by TP.
CC The present sequence represents a T. pallidum subspecies pertenue
CC (CDC-2) arp protein.
XX
SQ Sequence 232 AA;
XX
Query Match 100.0%; Score 101; DB 22; Length 232;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 EVEDVPKVVPEPASEREGGER 20
DB 128 EVEDVPKVVPEPASEREGGER 147
XX
RESULT 3
AAB48318
ID AAB48318 standard; Protein; 312 AA.
XX
AC AAB48318;
XX
DT 20-APR-2001 (first entry)
XX
DE T. pallidum ssp. endemicum (Bosnia) acidic repeat protein (arp).
XX
KW Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;
KW yaws; bejel.
XX
OS Treponema pallidum ssp. endemicum.
XX
PN WO200077486-A2.
XX
PD 21-DEC-2000.
XX
XX 14-JUN-2000; 2000MO-US16425.
PF
XX 14-JUN-1999; 99US-0138981.
PR
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX Liu H, Steiner B, Rhodes B;
PI
XX WPI; 2001-080711/09.
DR
XX N-PSDB; AAC84649.
XX
PT Detecting Treponema pallidum in blood, saliva, etc., by detecting
PT formation of a complex between immunogenic peptides of acidic repeat
PT protein of the bacterium and an antibody present in the biological
PT sample -
XX
XX Claim 15; Fig 10; 73pp; English.
XX
CC The invention relates to a method of detecting presence of Treponema
CC pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological
CC sample that involves contacting an acidic repeat protein (arp), or one
CC or more isolated immunogenic TP peptides of arp with an Ab containing
CC biological sample and then detecting the formation of a complex between
CC immunogenic peptides and Ab. The presence of the complex indicates the
CC presence of TP. The method is thus useful for diagnosing syphilis, yaws,
CC and bejel diseases. The immunogenic peptides or the Abs raised against
CC arp, as part of an immunogenic composition, are useful for inducing a
CC protective immune response against syphilis, yaws or bejel caused by TP.
CC The present sequence represents a T. pallidum subspecies endemicum
CC (Bosnia) arp protein.
XX
SQ Sequence 312 AA;
XX
Query Match 100.0%; Score 101; DB 22; Length 312;
Best Local Similarity 100.0%; Pred. No. 7e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 EVEDVPKVVPEPASEREGGER 20

DB 128 EVEDVPKVVPEPASREGER 147

RESULT 4

AA848316 standard; Protein; 432 AA.

AC AA848316;

DT 20-APR-2001 (first entry)

DE T. pallidum ssp. pallidum (Ni) acidic repeat protein (arp).

KW Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis; yaws; bejel.

OS Treponema pallidum ssp. pallidum.

PN WO200077486-A2.

PD 21-DEC-2000.

PF 14-JUN-2000; 2000WO-US16425.

PR 14-JUN-1999; 99US-0138981.

PS (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Liu H, Steiner B, Rhodes B;

DR WPI; 2001-080711/09.

DR N-PSDB; AAC84647.

PT Detecting Treponema pallidum in blood, saliva, etc., by detecting formation of a complex between immunogenic peptides of acidic repeat protein of the bacterium and an antibody present in the biological sample -

PS Claim 15; Fig 6; 73pp; English.

CC The invention relates to a method of detecting presence of Treponema pallidum (TP), anti-Treponemal antibodies (Abs), or both in a biological sample that involves contacting an acidic repeat protein (arp), or one or more isolated immunogenic TP peptides of arp with an Ab containing biological sample and then detecting the formation of a complex between immunogenic peptides and Ab. The presence of the complex indicates the presence of TP. The method is thus useful for diagnosing syphilis, yaws, and bejel diseases. The immunogenic peptides or the Abs raised against arp, as part of an immunogenic composition, are useful for inducing a protective immune response against syphilis, yaws or bejel caused by TP. CC The present sequence represents a T. pallidum subspecies pallidum (Ni) arp protein.

SQ Sequence 432 AA;

Query Match 100.0%; Score 101; DB 22; Length 432;

Best Local Similarity 100.0%; Pred. No. 1e-07; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVEDVPKVVPEPASREGER 20

DB 168 EVEDVPKVVPEPASREGER 187

RESULT 5

AA848329 standard; peptide; 20 AA.

AC AA848329;

DT 20-APR-2001 (first entry)

DE T. pallidum acidic repeat protein immunogenic peptide arp 11.

KW Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis; yaws; bejel.

OS Treponema pallidum.

PN WO200077486-A2.

PD 21-DEC-2000.

PF 14-JUN-2000; 2000WO-US16425.

PR 14-JUN-1999; 99US-0138981.

PS (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Liu H, Steiner B, Rhodes B;

DR WPI; 2001-080711/09.

PT Detecting Treponema pallidum in blood, saliva, etc., by detecting formation of a complex between immunogenic peptides of acidic repeat protein of the bacterium and an antibody present in the biological sample -

PS Claim 15; Fig 11; 73pp; English.

CC The invention relates to a method of detecting presence of Treponema pallidum (TP), anti-Treponemal antibodies (Abs), or both in a biological sample that involves contacting an acidic repeat protein (arp), or one or more isolated immunogenic TP peptides of arp with an Ab containing biological sample and then detecting the formation of a complex between immunogenic peptides and Ab. The presence of the complex indicates the presence of TP. The method is thus useful for diagnosing syphilis, yaws, and bejel diseases. The immunogenic peptides or the Abs raised against arp, as part of an immunogenic composition, are useful for inducing a protective immune response against syphilis, yaws or bejel caused by TP. CC Sequences AA848319-AA848330 represent immunogenic peptides of T. pallidum arp protein.

SQ Sequence 20 AA;

Query Match 96.0%; Score 97; DB 22; Length 20;

Best Local Similarity 95.0%; Pred. No. 1.4e-08; Mismatches 1; Indels 0; Gaps 0;

OY 1 EVEDVPKVVPEPASREGER 20

DB 1 EVEDVPKVVPEPASREGER 20

RESULT 6

AA848328 standard; peptide; 20 AA.

AC AA848328;

DT 20-APR-2001 (first entry)

DE T. pallidum acidic repeat protein immunogenic peptide arp 10.

KW Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis; yaws; bejel.

OS Treponema pallidum.

PN WO200077486-A2.

PD 21-DEC-2000.

PF 14-JUN-2000; 2000WO-US16425.

```

RR      14-JUN-1999;      99US-0138981.
XX
XX      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA
PI      Liu H, Steiner B, Rhodes B;
XX
XX      WPI; 2001-080711/09.
XX
XX      Detecting Treponema pallidum in blood, saliva, etc., by detecting
PT      formation of a complex between immunogenic peptides of acidic repeat
PT      protein of the bacterium and an antibody present in the biological
PT      sample -
XX
XX      Claim 15; Fig 11; 73pp; English.
PS
XX
XX      The invention relates to a method of detecting presence of Treponema
CC      pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological
CC      sample that involves contacting an acidic repeat protein (arp), or one
CC      or more isolated immunogenic TP peptides of arp with an Ab containing
CC      biological sample and then detecting the formation of a complex between
CC      immunogenic peptides and Ab. The presence of the complex indicates the
CC      presence of TP. The method is thus useful for diagnosing syphilis, yaws,
CC      and bejel diseases. The immunogenic peptides or the Abs raised against
CC      arp, as part of an immunogenic composition, are useful for inducing a
CC      protective immune response against syphilis, yaws or bejel caused by TP.
CC      Sequences AAB84319-AAB48330 represent immunogenic peptides of T. pallidum
CC      arp protein.
XX
XX      Sequence      20 AA;
SQ
XX
XX      Query Match      95.0%;      Score 96;      DB 22;      Length 20;
XX      Best Local Similarity      95.0%;      Pred. No. 2e-08;
XX      Matches      19;      Conservative      1;      Mismatches      0;      Indels      0;      Gaps      0;
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XX      1      EVEDPKYVEPASEREGGER      20
XX      1      EYENVPKVEPASEREGGER      20
XX
XX      Db
XX
XX      RESULT 7
XX      AAB48320
XX      ID. AAB48320 standard; peptide; 20 AA.
XX
XX      AAB48320;
XX
XX      20-APR-2001 (first entry)
XX
XX      T. pallidum acidic repeat protein immunogenic peptide arp 2.
XX
XX      Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;
XX      yaws; bejel.
XX
XX      Treponema pallidum.
XX
XX      WO200077486-A2.
XX
XX      21-DEC-2000.
XX
XX      14-JUN-2000; 2000MO-US16425.
XX
XX      14-JUN-1999; 99US-0138981.
XX
XX      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX      Liu H, Steiner B, Rhodes B;
XX
XX      WPI; 2001-080711/09.
XX
XX      Detecting Treponema pallidum in blood, saliva, etc., by detecting
PT      formation of a complex between immunogenic peptides of acidic repeat
PT      protein of the bacterium and an antibody present in the biological
PT      sample -
XX

```

S6	Claim 15; Fig 11; 73pp; English.
XX	The invention relates to a method of detecting presence of Treponema pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological sample that involves contacting an acidic repeat protein (arp), or one or more isolated immunogenic TP peptides of arp with an Ab containing immunogenic peptide and then detecting the formation of a complex between immunogenic peptide and Ab. The presence of the complex indicates the presence of TP. The method is thus useful for diagnosing syphilis, yaws, and bejel diseases. The immunogenic peptides or the Abs raised against arp, as part of an immunogenetic composition, are useful for inducing a protective immune response against syphilis, yaws or bejel caused by TP. Sequences AAB48319-AAB48330 represent immunogenic peptides of T. pallidum arp protein.
CC	
CC	
CQ	Sequence 20 AA;
Query Match	86.1%; Score 87; DB 22; Length 20;
Best Local Similarity	94.4%; Pred. No. 5,4e-07;
Matches 17; Conservative	0; Mismatches 1; Gaps 0;
Oy	1 EVEDVPKVEPASEREGG 18 Db 3 EVEDAPKVPEPASREGG 20
RESULT 8	
AAB48330 ID	AAB48330 standard; peptide: 20 AA.
AC AAB48330,	
AD 20-APR-2001	(first entry)
DE T. pallidum acidie repeat protein immunogenic peptide arp 12.	
KW Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis; yaws; bejel.	
XN Treponema pallidum.	
PV WO200077486-A2.	
PD 21-DEC-2000.	
PF 14-JUN-2000; 2000WO-US16425.	
PR 14-JUN-1999; 99US-0138981.	
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.	
PI Liu H, Steiner B, Rhodes B;	
DZ WPI; 2001-080711/09.	
DR	
DT Detecting Treponema pallidum in blood, saliva, etc., by detecting formation of a complex between immunogenic peptides of acidic repeat protein of the bacterium and an antibody present in the biological sample -	
PS Claim 15; Fig 11; 73pp; English.	
XX	The invention relates to a method of detecting presence of Treponema pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological sample that involves contacting an acidic repeat protein (arp), or one or more isolated immunogenic TP peptides of arp with an Ab containing immunogenic peptide and then detecting the formation of a complex between immunogenic peptide and Ab. The presence of the complex indicates the presence of TP. The method is thus useful for diagnosing syphilis, yaws, and bejel diseases. The immunogenic peptides or the Abs raised against arp, as part of an immunogenetic composition, are useful for inducing a protective immune response against syphilis, yaws or bejel caused by TP. Sequences AAB48319-AAB48330 represent immunogenic peptides of T. pallidum

OS Treponema pallidum.
XX
PN WO200077486-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US16425.
XX
PR 14-JUN-1999; 99US-0138981.
XX
PS (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Liu H, Steiner B, Rhodes B;
XX
DR WPI; 2001-080711/09.
XX
PT Detecting Treponema pallidum in blood, saliva, etc., by detecting
PT formation of a complex between immunogenic peptides of acidlic repeat
PT protein of the bacterium and an antibody present in the biological
PT sample -
XX
PS Claim 15; Fig 11; 73pp; English.
XX
CC The invention relates to a method of detecting presence of Treponema
CC pallidum (TP), anti-Treponemal antibodies (Abs), or both in a biological
CC sample that involves contacting an acidlic repeat protein (arp), or one
CC or more isolated immunogenic TP peptides of arp with an Ab containing
CC biological sample and then detecting the formation of a complex between
CC immunogenic peptides and Ab. The presence of the complex indicates the
CC presence of TP. The method is thus useful for diagnosing syphilis, yaws,
CC and bejel diseases. The immunogenic peptides or the Abs raised against
CC arp, as part of an immunogenic composition, are useful for inducing a
CC protective immune response against syphilis, yaws or bejel caused by TP.
CC Sequences AAB48319-AAB48330 represent immunogenic peptides of T. pallidum
CC arp protein.
XX
SQ Sequence 19 AA;
XX
Query Match 59.4%; Score 60; DB 22; Length 19;
Best Local Similarity 92.3%; Pred. No. 0.011; Mismatches 1; Indels 0; Gaps 0;
Matches 12; Conservative 0;
XX
QY 1 EVEDVKKVVEPAS 13
DB 7 EVEDAKVVEPAS 19
XX
RESULT 12
AAB48326
ID AAB48326 standard; peptide; 26 AA.
XX
AC AAB48326;
XX
DT 20-APR-2001 (first entry)
XX
DE T. pallidum acidlic repeat protein immunogenic peptide arp 8.
XX
KM Treponema pallidum, acidlic repeat protein; arp; immunogenic; syphilis;
KM yaws; bejel.
XX
OS Treponema pallidum.
XX
PN WO200077486-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US16425.
XX
PR 14-JUN-1999; 99US-0138981.
XX
PS (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Liu H, Steiner B, Rhodes B;

XX
DR WPI; 2001-080711/09.
XX
PT Detecting Treponema pallidum in blood, saliva, etc., by detecting
PT formation of a complex between immunogenic peptides of acidlic repeat
PT protein of the bacterium and an antibody present in the biological
PT sample -
XX
PS Claim 15; Fig 11; 73pp; English.
XX
CC The invention relates to a method of detecting presence of Treponema
CC pallidum (TP), anti-Treponemal antibodies (Abs), or both in a biological
CC sample that involves contacting an acidlic repeat protein (arp), or one
CC or more isolated immunogenic TP peptides of arp with an Ab containing
CC biological sample and then detecting the formation of a complex between
CC immunogenic peptides and Ab. The presence of the complex indicates the
CC presence of TP. The method is thus useful for diagnosing syphilis, yaws,
CC and bejel diseases. The immunogenic peptides or the Abs raised against
CC arp, as part of an immunogenic composition, are useful for inducing a
CC protective immune response against syphilis, yaws or bejel caused by TP.
CC Sequences AAB48319-AAB48330 represent immunogenic peptides of T. pallidum
CC arp protein.
XX
SQ Sequence 26 AA;
XX
Query Match 52.5%; Score 53; DB 22; Length 26;
Best Local Similarity 84.6%; Pred. No. 0.21; Mismatches 2; Indels 0; Gaps 0;
Matches 11; Conservative 0;
XX
QY 8 VVEPASEREGGER 20
DB 1 VVEPASGHEGGER 13
XX
RESULT 13
AAG61691
ID AAG61691 standard; Protein; 79 AA.
XX
AC AAG61691;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 80063.
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KM Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
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 XX Arabidopsis thaliana.
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Search completed: August 1, 2003, 18:27:25
Job time : 43 secs

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